

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:39:22 ; Search time 49 Seconds
(without alignments)
2056.099 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPOKTFGELKNLPL.....RLWLQLEKGRYAKDVWAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR-73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1049	1 A34286	NADPH-ferrihemopro
2	28	2.7	1054	1 A69975	NADPH-ferrihemopro
3	21	2.0	1061	2 D69799	Cytochrome P450 /
4	16	1.5	661	2 T40056	nadh-cytochrome p
5	16	1.5	678	1 S29123	NADPH-ferrihemopro
6	15	1.4	693	1 S38427	NADPH-ferrihemopro
7	13	1.2	558	2 T37567	probable NADPH cyt
8	13	1.2	605	1 G70040	sulfite reductase
9	13	1.2	607	2 A83726	sulfite reductase
10	13	1.2	710	2 JC7192	NADPH-ferrihemopro
11	12	1.1	677	1 RDPG04	NADPH-ferrihemopro
12	12	1.1	677	2 A60557	NADPH-ferrihemopro
13	12	1.1	678	2 S27158	NADPH-ferrihemopro
14	12	1.1	679	2 A25505	NADPH-ferrihemopro
15	12	1.1	691	1 S46735	NADPH-ferrihemopro
16	11	1.0	506	2 S37156	NADPH-ferrihemopro
17	11	1.0	681	2 T14903	NADPH-ferrihemopro
18	11	1.0	690	2 A47298	NADPH-ferrihemopro
19	11	1.0	692	2 T05582	NADPH-ferrihemopro
20	11	1.0	692	2 S37159	NADPH-ferrihemopro
21	11	1.0	693	2 T14904	NADPH-ferrihemopro
22	10	1.0	238	2 T10771	NADPH-ferrihemopro
23	10	1.0	571	2 T39378	probable FAD bindi
24	10	1.0	590	2 S37157	NADPH-ferrihemopro
25	10	1.0	601	2 A28577	NADPH-ferrihemopro
26	10	1.0	612	2 G82674	NADPH-sulfite redu
27	10	1.0	614	2 B82329	sulfite reductase
28	10	1.0	683	2 T10720	NADPH-ferrihemopro
29	10	1.0	1429	2 JN0609	nitric-oxide synth

30	10	1.0	1429	2 S16233	nitric-oxide synth
31	10	1.0	1433	2 G01946	nitric-oxide synth
32	9	0.9	327	2 S53305	ferredoxin-NADP re
33	9	0.9	375	2 T02215	ferredoxin-NADP re
34	9	0.9	378	1 T03758	probable ferredoxi
35	9	0.9	489	2 T06715	probable cytochrom
36	9	0.9	671	2 A56592	NADPH-ferrihemopro
37	9	0.9	680	2 S63895	NADPH-ferrihemopro
38	9	0.9	680	2 S63698	NADPH-ferrihemopro
39	9	0.9	680	2 A37890	NADPH-ferrihemopro
40	9	0.9	705	2 T10723	NADPH-ferrihemopro
41	9	0.9	1144	1 A43271	nitric-oxide synth
42	9	0.9	1147	1 S47647	nitric-oxide synth
43	9	0.9	1147	1 I56575	nitric-oxide synth
44	9	0.9	1147	1 S38253	nitric-oxide synth
45	9	0.9	1147	1 I53165	nitric-oxide synth

ALIGNMENTS

RESULT 1

A34286

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium

N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (

C:Species: Bacillus megaterium

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002

C:Accession: A34286; S43653

R:Ruettinger, R.T.; Wen, L.P.; Fulco, A.J.

J. Biol. Chem. 264, 10987-10995, 1989

A:Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-

A:Reference number: A34286; MUID:89291834; PMID:2544578

A:Accession: A34286

A:Molecule type: DNA

A:Residues: 1-1049 <RUE>

A:Cross-references: GB:J04832; NID:g142797; PIDN:AAA87602.1; PID:g142798

R:Munro, A.W.; Lindqvist, J.G.; Coggins, J.R.; Kelly, S.M.; Price, N.C.

FEBS Lett. 343, 70-74, 1994

A:Title: Structural and enzymological analysis of the interaction of isolated domains

A:Reference number: S43653; MUID:94215710; PMID:8163021

A:Accession: S43653

A:Molecule type: protein

A:Residues: 430-439; 441-496 <MUN>

C:Genetics:

A:Gene: CYP102

C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin

C:Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met

F:262-423/Domain: cytochrome P450 homology <P45>

F:483-1046/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:485-622/Domain: flavodoxin homology <FLX>

F:401/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 1048; DB 1; Length 1049;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRVYLSORLIKE	60
Db	2	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRVYLSORLIKE	61
Qy	61	ACDSRFDKNSLQALKFVRDFAGDGLFTSWTHENKWKKAHNILLPSFSQAMKGYHAMV	120
Db	62	ACDSRFDKNSLQALKFVRDFAGDGLFTSWTHENKWKKAHNILLPSFSQAMKGYHAMV	121
Qy	121	DIADVQVQKWERLNADEHIEVPEDWTRLTLDITGLCGFNFRNFYRDPHPFITSMVRA	180
Db	122	DIADVQVQKWERLNADEHIEVPEDWTRLTLDITGLCGFNFRNFYRDPHPFITSMVRA	181
Qy	181	LDEAMNKLQRPNDPPAYDENKROFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG	240
Db	182	LDEAMNKLQRPNDPPAYDENKROFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG	241
Qy	241	KDPTGEPDLDENIRYQIITFLIAGHETTSGLLSFALYFLVKPNHVLQKAAEAARVLVD	300

Db 242 KDPETGEPLDENIRYQITFLAGHETTSGLSFALYFLVKNPHVYLRKAAEEAARVLVD 301
QY 301 PVPYSYQVQKLVGVVNLALRLWTPAFSLYAKEDTVLGGEYPLEKGDDELWLIPQL 360
Db 302 PVPYSYQVQKLVGVVNLALRLWTPAFSLYAKEDTVLGGEYPLEKGDDELWLIPQL 361
QY 361 HRDKTIWGDVVEFRPERFENPSPAIPOHAFKPFNGQQRACIGQOFALHEATLVGLMMLKH 420
Db 362 HRDKTIWGDVVEFRPERFENPSPAIPOHAFKPFNGQQRACIGQOFALHEATLVGLMMLKH 421
QY 421 FDFEDHTNYELDIKETLTKPEGVVYKAKSKTIPLGGIPSPSTEQSAKVKRKAENAHNT 480
Db 422 FDFEDHTNYELDIKETLTKPEGVVYKAKSKTIPLGGIPSPSTEQSAKVKRKAENAHNT 481
QY 481 PLVLVGSNMGTAEGTARDLADTAMSGKFAPOQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 482 PLVLVGSNMGTAEGTARDLADTAMSGKFAPOQVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLQASADEYKGVYRVSFGCGDKNWTYQKVPFADITETLAARGAENIADR 600
Db 542 PDNAKQFVDWLQASADEYKGVYRVSFGCGDKNWTYQKVPFADITETLAARGAENIADR 601
QY 601 GEADASDDFEGTYEENREHWSVAAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADASDDFEGTYEENREHWSVAAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 661
QY 661 AFSTNVVASKELQPGQSASTRHLEIETLPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 720
Db 662 AFSTNVVASKELQPGQSASTRHLEIETLPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 721
QY 721 DASQQLRLAEKLAHLPLAKTVSVVEILLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQLRLAEKLAHLPLAKTVSVVEILLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLEKQAKQVLAERLWLELLEKYPACEMKFEFIALLSIRPRYYSISSSPVDEK 840
Db 782 EALLEKQAKQVLAERLWLELLEKYPACEMKFEFIALLSIRPRYYSISSSPVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITFCISPPQSEFTLPKDPPEPLIM 900
Db 842 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITFCISPPQSEFTLPKDPPEPLIM 901
QY 901 VPGTGVAPFGRVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 902 VPGTGVAPFGRVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVENTLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVENTLMKSYADV 1021
QY 1021 HQVSEADARLWLOLEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOLEKGRYAKDVWAG 1049

RESULT 2

A69975
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus subtilis
N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC
C:Species: Bacillus subtilis
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Jun-2002
C:Accession: A69975
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrar, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69975
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1054 <KUN>
A:Cross-references: GB:299117; GB:AL009126; NID:G2634966; PID:G2635162
A:Experimental source: strain 168
C:Genetics:
A:Gene: yrhJ
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; monooxygenase; o
F:486-1050/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:488-625/Domain: flavodoxin homology <FLX>
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted
Query Match 2.7%; Score 28; DB 1; Length 1054;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 249 LDENIRYQITFLIAGHETTSGLSFA 276
Db 252 LDENIRYQITFLIAGHETTSGLSFA 279
RESULT 3
D69799
cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Accession: D69799
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrar, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69799
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1061 <KUN>
A:Cross-references: GB:299107; GB:AL009126; NID:G2632866; PIDN:CAB12544.1; PID:G26330
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeto
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein
F:264-425/Domain: cytochrome P450 homology <P45>
F:493-1057/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:495-632/Domain: flavodoxin homology <FLX>
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted
Query Match 2.0%; Score 21; DB 2; Length 1061;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 DMTRLTDTIGLCGNGYRNS 164
Db 146 DMTRLTDTIGLCGNGYRNS 166

RESULT 4

T40056
nadh-cytochrome p450 reductase - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C;Accession: T40056
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21903
A;Accession: T40056
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-661 <LYN>
A;Cross-references: EMBL:AL034463; PIDN:CAA22429.1; GSPDB:GN00067; SPDB:SPBC29A10.01
A;Experimental source: strain 972h-; cosmid c29A10
C;Genetics:
A;Gene: SPDB:SPBC29A10.01
A;Map position: 2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein
C;Keywords: flavoprotein

Query Match 1.5%; Score 16; DB 2; Length 661;

Best Local Similarity 100.0%; Pred. No. 6.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 IMVGGTGVAPFRGFV 914

|||||

Db 517 IMVGGTGVAPFRGFV 532

RESULT 5

S29123
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: NADP-cytochrome P450 reductase
C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: S29123; S20814
R;Miles, J.S.
Biochem. J. 287, 195-200, 1992
A;Title: Structurally and functionally conserved regions of cytochrome P-450 reductase a
saccharomyces pombe cDNA.
A;Reference number: S29123; MUID:93038553; PMID:1417773.
A;Accession: S29123
A;Molecule type: mRNA
A;Residues: 1-678 <MIL>
A;Cross-references: EMBL:X64702; NID:g4943; PIDN:CAA45956.1; PID:g4944
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21920
A;Accession: T40324
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-678 <WOO>
A;Cross-references: EMBL:AL078627; PIDN:CAB44769.1; GSPDB:GN00067; SPDB:SPBC365.17
A;Experimental source: strain 972h-; cosmid c365
C;Genetics:
A;Gene: SPBC365.17
A;Map position: 2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; membrane F
F;53-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;55-208/Domain: flavodoxin homology <FLX>

Query Match 1.5%; Score 16; DB 1; Length 678;

Best Local Similarity 100.0%; Pred. No. 6.9e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 IMVGGTGVAPFRGFV 914

|||||

Db 534 IMVGGTGVAPFRGFV 549

RESULT 6

S38427
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger
N;Alternate names: NADPH-cytochrome P450 oxidoreductase
C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: S38427
R;van den Brink, J.; van Zeijl, C.; van den Hondel, C.; van Gorcom, R.
submitted to the EMBL Data Library, October 1993
A;Description: Cloning and characterization of the NADPH cytochrome P450 oxidoreducta
A;Reference number: S38427
A;Accession: S38427
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-693 <VAN>
A;Cross-references: EMBL:Z26938; NID:g408110; PIDN:CAA81550.1; PID:g408111
C;Genetics:
A;Introns: 595/3
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein; NADP; oxidoreductase
C;Keywords: NADPH-ferrihemoprotein reductase homology <FEH>
F;66-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;68-220/Domain: flavodoxin homology <FLX>

Query Match 1.4%; Score 15; DB 1; Length 693;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 IMVGGTGVAPFRGF 913

|||||

Db 544 IMVGGTGVAPFRGF 558

RESULT 7

T37567
probable NADPH cytochrome reductase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: T37567
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21725
A;Accession: T37567
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-558 <WOO>
A;Cross-references: EMBL:AL035439; PIDN:CAB36512.2; GSPDB:GN00066; SPDB:SPAC1296.06
A;Experimental source: strain 972h-; cosmid c1296
C;Genetics:
A;Gene: SPDB:SPAC1296.06
A;Map position: 1
A;Introns: 45/3; 71/3; 111/2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein

Query Match 1.2%; Score 13; DB 2; Length 558;

Best Local Similarity 100.0%; Pred. No. 0.00052;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 897 PLIMVGGTGVAP 909

|||||

Db 414 PLIMVGGTGVAP 426

RESULT 8

G70040
sulfite reductase (NADPH2) (EC 1.8.1.2) flavoprotein yvgr - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: G70040
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueed, Y., M.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Authors: Schleich, S.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; PMID:98044033; PMID:9384377
A:Accession: G70040
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-605 <KUN>
A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CABL5349.1; PID:g2635857
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvgr
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein reductase
C:Keywords: flavoprotein; NADP: oxidoreductase
F:58-604/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:70-209/Domain: flavodoxin homology <FLX>

Query Match 1.2%; Score 13; DB 1; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPFR 911
Db 462 IMVGPCTGVAPFR 474
|||||

RESULT 9
A83726
sulfite reductase (NADPH) BH0609 [Imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-May-2002
C:Accession: A83726
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; PMID:20512582; PMID:11058132
A:Accession: A83726
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-607 <STO>
A:Cross-references: GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BAB04328.1; GSPDB:GN0
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0609
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein re
C:Keywords: flavoprotein

Query Match 1.2%; Score 13; DB 2; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPFR 911
Db 464 IMVGPCTGVAPFR 476
|||||

RESULT 10
JC7192
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Cunninghamella elegans
C:Species: Cunninghamella elegans
C>Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 03-Jun-2002
C:Accession: JC7192
R:Yadav, J.S.; Loper, J.C.
Biochem. Biophys. Res. Commun. 268, 345-353, 2000

A:Title: Cloning and characterization of the cytochrome P450 oxidoreductase gene from
A:Reference number: JC7192; PMID:20145435; PMID:10679206
A:Accession: JC7192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-710 <YAD>
A:Cross-references: GB:AF195659
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem
C:Keywords: flavoprotein; oxidoreductase

Query Match 1.2%; Score 13; DB 2; Length 710;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAPFRGFV 914
Db 564 GPGTGVAPFRGFV 576
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RESULT 11 RDPG04

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig
N:Alternate names: NADP-cytochrome P450 reductase
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 04-Dec-1986 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C:Accession: A25584; A00403
R:Haniu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.
Biochemistry 25, 7906-7911, 1986
A:Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcine
A:Reference number: A25584; PMID:87101085; PMID:3099837
A:Accession: A25584
A:Molecule type: protein
A:Residues: 1-677 <HAN>
R:Vogel, F.; Lumpkin, L.
Biochem. J. 236, 871-878, 1986
A:Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome
A:Reference number: A00403; PMID:87075664; PMID:3098240
A:Accession: A00403
A:Molecule type: protein
A:Residues: 56-162 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem
C:Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav
F:76-126/Domain: FMN binding <FMN>
F:79-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:81-223/Domain: Flavodoxin homology <FLX>
F:451-476/Domain: FAD binding <FAD>
F:1/Modified site: acetylated amino end (Gly) #status experimental

Query Match 1.1%; Score 12; DB 1; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPFR 910
Db 528 IMVGPCTGVAPFR 539
|||||

RESULT 12

A60557
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - human
N:Alternate names: NADP-cytochrome P450 reductase
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C:Accession: A33421; A60557; S21686
R:Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.
Biochemistry 28, 8639-8645, 1989
A:Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from
A:Reference number: A33421; PMID:90105390; PMID:2513880
A:Accession: A33421
A:Molecule type: protein
A:Residues: 2-677 <HAN>
A>Note: 551-Gln was also found
R:Yamano, S.; Aoyama, T.; McBride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J

Mol. Pharmacol. 36, 83-88, 1989
 A;Title: Human NADPH-P450 oxidoreductase: complementary DNA cloning, sequence and vaccination
 A;Reference number: A60557; MUID:89313720; PMID:2501655
 A;Accession: A60557
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137, 'G', 139-577, 'DV', 580-677 <YAM>
 R;Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.
 Arch. Biochem. Biophys. 294, 168-172, 1992
 A;Title: Quantification of cytochrome P450 reductase gene expression in human tissues.
 A;Reference number: S21686; MUID:92198003; PMID:1550342
 A;Accession: S21686
 A;Molecule type: mRNA
 A;Residues: 2-499, 'V', 501-517, 'L', 519-536, 'WH', 539-677 <SHE>
 A;Cross-references: GB:S90469; NID:9247306; PIDN:AB21814.1; PID:9247307
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
 C;Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flavoprotein
 F;1-56/Domain: membrane-bound #status predicted <MEM>
 F;2-677/Product: NADPH-ferrihemoprotein reductase #status experimental <MAT>
 F;77-227/Domain: FMN binding #status predicted <FMN>
 F;80-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;82-224/Domain: flavodoxin homology <FLX>
 F;84-95/Region: FMN-phosphate binding #status predicted
 F;267-326/452-477/Domain: FAD binding #status predicted <FAD>
 F;293-296/Region: FAD-pyrophosphate binding #status predicted
 F;2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
 F;566/Binding site: NADP (Cys) #status experimental

Query Match 1.1%; Score 12; DB 2; Length 677;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910
 Db 529 IMVPGTGVAPF 540
 |||||

RESULT 13
 S27158
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - guinea pig
 N;Alternate names: NADPH-cytochrome P450 oxidoreductase
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
 C;Accession: S27158; S38510
 R;Ohgiya, S.; Goda, T.; Ishizaki, K.; Kamataki, T.; Shinriki, N.
 Biochim. Biophys. Acta 1171, 103-105, 1992
 A;Title: Molecular cloning and sequence analysis of mouse NADPH-cytochrome P-450 oxidoreductase
 A;Reference number: S27158; MUID:93041995; PMID:1420354
 A;Accession: S27158
 A;Molecule type: mRNA
 A;Residues: 1-678 <OHG>
 A;Cross-references: EMBL:D10498; NID:9220556; PIDN:BAA01385.1; PID:9220557
 A;Note: the species identification has been revised in reference S38510
 R;Ohgiya, S.; Goda, T.; Ishizaki, K.; Kamataki, T.; Shinriki, N.
 Biochim. Biophys. Acta 1174, 313, 1993
 A;Reference number: S38510; MUID:93385164; PMID:8373812
 A;Contents: annotation; erratum
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
 C;Keywords: electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; NADP; oxidoreductase
 F;79-188/Domain: FMN binding #status predicted <FMN>
 F;80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;82-224/Domain: flavodoxin homology <FLX>
 F;292-326,454-477/Domain: FAD binding #status predicted <FAD>

Query Match 1.1%; Score 12; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910
 Db 529 IMVPGTGVAPF 540
 |||||

RESULT 14
 A25505
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 03-Jun-2002
 C;Accession: A25505; A05233
 R;Katagiri, M.; Murakami, H.; Yabusaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Ohgiya, S.
 J. Biochem. 100, 945-954, 1986
 A;Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver NADPH-ferrihemoprotein reductase
 A;Reference number: A25505; MUID:87137361; PMID:3029050
 A;Accession: A25505
 A;Molecule type: mRNA
 A;Residues: 1-679 <KAT>
 A;Cross-references: GB:X04610; NID:91543; PIDN:CAA28279.1; PID:91544
 R;Black, S.D.; Coon, M.J. 5938, 1982
 J. Biol. Chem. 257, 5923-5938, 1982
 A;Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hy
 A;Reference number: A05233; MUID:82167456; PMID:6802823
 A;Accession: A05233
 A;Molecule type: protein
 A;Residues: 1-679, 'NY', 42-52, 'N', 54-81 <BLA>
 A;Note: the order of the first four residues was not determined
 A;Note: the amino end of the mature protein is acetylated
 C;Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
 C;Keywords: acetylated amino end; electron transfer; FAD; flavoprotein; FMN; membrane
 F;1-56/Domain: membrane-bound #status predicted <MEM>
 F;78-228/Domain: FMN binding #status predicted <FMN>
 F;81-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;83-225/Domain: flavodoxin homology <FLX>
 F;85-96/Region: FMN-phosphate binding #status predicted
 F;268-327,453-478/Domain: FAD binding #status predicted <FAD>
 F;294-297/Region: FAD-pyrophosphate binding #status predicted

Query Match 1.1%; Score 12; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910
 Db 530 IMVPGTGVAPF 541
 |||||

RESULT 15
 S46735
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - yeast (Saccharomyces cerevisiae)
 N;Alternate names: NADP-cytochrome P450 reductase; protein H8179.8; protein YHR042w
 C;Species: Saccharomyces cerevisiae
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 C;Accession: S46735; A41447; B41447
 R;Du, Z.
 submitted to the EMBL Data Library, May 1994
 A;Description: The sequence of S. cerevisiae cosmid 8179.
 A;Reference number: S46732
 A;Accession: S46735
 A;Molecule type: DNA
 A;Residues: 1-691 <DUZ>
 A;Cross-references: EMBL:U00062; NID:9488162; PIDN:AAB68904.1; PID:9488169; GSPDB:GNO
 R;Yabusaki, Y.; Murakami, H.; Ohkawa, H.
 J. Biochem. 103, 1004-1010, 1988
 A;Title: Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450 reductas
 A;Reference number: A41447; MUID:89008184; PMID:3139648
 A;Accession: A41447
 A;Molecule type: DNA
 A;Residues: 1-422, 'N', 424-473, 'G', 475-691 <YAB>
 A;Cross-references: GB:D13788; GB:D00316; NID:9218452; PIDN:BAA02936.1; PID:9218453
 A;Accession: B41447
 A;Molecule type: protein
 A;Residues: 2-13,45-62 <YAZ>
 C;Genetics:
 A;Gene: SGD:NCPI; PRD1; SGD:S0001084
 A;Cross-references: MIPS:YHR042w; SGD:S0001084
 A;Map position: 8R

C;Function:
A;Description: electron transfer; oxidoreductase
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase
C;Keywords: electron transfer; endoplasmic reticulum; flavoprotein; NADP; oxidoreductase
F;61-690/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;63-204/Domain: flavodoxin homology <FLX>

Query Match 1.1%; Score 12; DB 1; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	902	GGGTGVAPFRGF	913
Db	540	GGGTGVAPFRGF	551

Search completed: May 29, 2003, 08:44:50
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:32:22 ; Search time 26 Seconds
(without alignments)
1671.815 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLOQEEKGRYAKDWWAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	1048	100.0	1048	1	CPXB_BACME
2	28	2.7	1034	1	CYPE_BACSU
3	21	2.0	1061	1	CYPD_BACSU
4	16	1.5	678	1	NCPR_SCHPO
5	12	1.1	676	1	NCPR_HUMAN
6	12	1.1	677	1	NCPR_CAVPO
7	12	1.1	677	1	NCPR_MOUSE
8	12	1.1	677	1	NCPR_PIG
9	12	1.1	679	1	NCPR_RABIT
10	12	1.1	690	1	NCPR_YEAST
11	11	1.0	690	1	NCPR_PHAU
12	10	1.0	571	1	YB63_SCHPO
13	10	1.0	601	1	NCPR_SALTR
14	10	1.0	1429	1	NOS1_MOUSE
15	10	1.0	1429	1	NOS1_RAT
16	10	1.0	1434	1	NOS1_HUMAN
17	10	1.0	1435	1	NOS1_RABIT
18	9	0.9	375	1	FENS_TOBAC
19	9	0.9	378	1	FENS_ORYSA
20	9	0.9	489	1	C71Q_ARATH
21	9	0.9	496	1	NOS2_RABIT
22	9	0.9	516	1	C4AD_DROME
23	9	0.9	671	1	NCPR_MUSDO
24	9	0.9	679	1	NCPR_DROME
25	9	0.9	680	1	NCPR_CANNA
26	9	0.9	680	1	NCPR_CANTR
27	9	0.9	1144	1	NOS2_MOUSE
28	9	0.9	1147	1	NOS2_RAT
29	9	0.9	1147	1	NS2D_HUMAN
30	9	0.9	1149	1	NS2D_CAVPO
31	9	0.9	1153	1	NOS_LYNST
32	8	0.8	200	1	VATE_BORBU
33	8	0.8	218	1	CP3J_CAPAE

RESULT 1

ID	CPXB_BACME	STANDARD;	PRT;	1048 AA.
AC	P14779;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450(BM-3))			
DE	(P450BM-3) [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-			
DE	cytochrome P450 reductase (EC 1.6.2.4)].			
GN	CYP102A1 OR CYP102.			
OS	Bacillus megaterium.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=99291834; PubMed=2544578;			
RA	Ruettinger R.T., Wen L.-P., Fulco A.J.;			
RT	"Coding nucleotide, 5' regulatory, and deduced amino acid sequences			
RT	of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450			
RT	reductase from Bacillus megaterium."			
RL	J. Biol. Chem. 264:10987-10995(1989).			
RN	[2]			
RP	CHARACTERIZATION.			
RP	MEDLINE=92088245; PubMed=1727637;			
RA	Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,			
RA	Peterson J.A.;			
RT	"Fatty acid monooxygenation by P450BM-3: product identification and			
RT	proposed mechanisms for the sequential hydroxylation reactions."			
RL	Arch. Biochem. Biophys. 292:20-28(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.			
RP	MEDLINE=93342510; PubMed=8342039;			
RA	Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,			
RA	Deisenhofer J.;			
RT	"Crystal structure of hemoprotein domain of P450BM-3, a prototype for			
RT	microsomal P450 s."			
RL	Science 261:731-736(1993).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.			
RP	MEDLINE=97185914; PubMed=9033595;			
RA	Li H.Y., Poulos T.L.;			
RT	"The structure of the cytochrome p450BM-3 haem domain complexed with			
RT	the fatty acid substrate, palmitoleic acid."			
RL	Nat. Struct. Biol. 4:140-146(1997).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 459-649.			
RP	MEDLINE=99162523; PubMed=10051560;			
RA	Sevrioukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;			
RT	"Structure of a cytochrome P450-redox partner electron-transfer			
RT	complex."			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.			
RP	MEDLINE=2152924; PubMed=11695892;			
RA	Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;			

P52056 synechocyst
Q06527 chromatium
P19649 treponema p
Q9v233 pyrococcus
Q9pgc5 xyliella fas
P18326 streptomyce
P26911 streptomyce
Q92r20 rhizobium m
P20815 homo sapien
P70795 agrobacteri
Q9sael arabidopsis
P51538 rattus norv

ALIGNMENTS

Db 421 DFEDHTNYELDIKETITLTKPEGVVVKAKSKKIPLGGIPSPTEQSAKVKRKAENAHNT 480
QY 481 PLVLVGSNMGTAEGTARDLADLAMSFGAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 481 PLVLVGSNMGTAEGTARDLADLAMSFGAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
QY 541 PDNAKQFVWLQDQASADEKGVRYVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600
Db 541 PDNAKQFVWLQDQASADEKGVRYVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600
QY 601 GEADASDDDEGTVEERHWSVDAAYFNLDIENSEDNKSTLSLQFVDSADNPLAKMHG 660
Db 601 GEADASDDDEGTVEERHWSVDAAYFNLDIENSEDNKSTLSLQFVDSADNPLAKMHG 660
QY 661 AFSTNVVASKELQPGSARSTRHLELPEKASVQSGDHLGVPRNVEGVNRTARFGL 720
Db 661 AFSTNVVASKELQPGSARSTRHLELPEKASVQSGDHLGVPRNVEGVNRTARFGL 720
QY 721 DASQQLRLAEKELHLPLAKTVSVVEELLYQVVELQDPTVTRTOLRAMAAKTVCPPHKVEL 780
Db 721 DASQQLRLAEKELHLPLAKTVSVVEELLYQVVELQDPTVTRTOLRAMAAKTVCPPHKVEL 780
QY 781 EALLEKQAYKEQVLAARLMLLELEKYPACEMKFSFIALLPSIRPRYYSISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAARLMLLELEKYPACEMKFSFIALLPSIRPRYYSISSPRVDEK 840
QY 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFPLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFPLPKDPETPLIM 900
QY 901 VGPCTGVAPRGVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 901 VGPCTGVAPRGVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
QY 961 HTAFSRMPNPKTYVQVHVMEQDKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQVHVMEQDKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
QY 1021 HQVSEADARLWLOQLEKGRYADVWAG 1048
Db 1021 HQVSEADARLWLOQLEKGRYADVWAG 1048

RESULT 2

TYPE_BACSU STANDARD; PRT; 1054 AA.
AC O08336:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)].
GN CYPE OR CYP102A3.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors Sigv and Sigz.";
RL Microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Besslerer P., Bolotin A., Borchert S.,

RA Boursier R., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.J., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Hollappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kunano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Priescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale I.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
CC -----
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CC -----
CC EMBL: U93874; AAB80867.1; -;
DR EMBL: Z99117; CAB14658.1; -;
DR HSSP: P14779; 1JPZ.
DR Subtilist; BG12299; cYPE.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00067; P450; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR Pfam: PF00258; flavodoxin; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
KW Complete proteome.
FT DOMAIN 1 475 CYTOCHROME P450.
FT DOMAIN 472 1053 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866C110 CRC64;
Query Match 2.7%; Score 28; DB 1; Length 1054;

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Best Local Similarity 100.0%; Pred. NO. 9.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LDDENRYQIITFLIAGHETTSGLLSFA 276
Db 252 LDDENRYQIITFLIAGHETTSGLLSFA 279

RESULT 3
CYPD_BACSU STANDARD; PRT; 1061 AA.
AC 008394;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)].
OS CYPD OR CYP102A2.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=93081178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors SigV and SigZ.";
RL Microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Fohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocycytochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +

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oxidized flavoprotein + H(2)O.
-1- COFACTOR: FAD AND FMN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
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EMBL; D87979; BAA20123.1; -.
DR EMBL; 299107; CAB12544.1; -.
DR HSSP; F14779; 1JFZ.
DR Subtilist; BG12871; cypD.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00067; P450; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
KW Complete proteome.
FT DOMAIN 1 474 CYTOCHROME P450.
FT DOMAIN 475 1061 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
SQ SEQUENCE 1061 AA; 119467 MW; 791SDACC20578978 CRC64;

Query Match 2.0%; Score 21; DB 1; Length 1061;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 DMTRLTDLTIGLCGFNYRFS 164
Db 146 DMTRLTDLTIGLCGFNYRFS 166

RESULT 4
NCPR_SCHPO STANDARD; PRT; 678 AA.
AC P36587; Q9USU6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN CCRI OR SPBC29A10.01 OR SPBC365.17.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93038553; PubMed=1417773;
RA Miles J.S.;
RT "Structurally and functionally conserved regions of cytochrome P-450
RT reductase as targets for DNA amplification by the polymerase chain
RT reaction. Cloning and nucleotide sequence of the Schizosaccharomycetes
RL pombe cDNA.";
RL Biochem. J. 287:195-200(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moulé S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicakert G., Aert R., Robben J., Grymonprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakowski G.V., Ussery D., Bartell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- COFACTOR: FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC -----
DR EMBL; X64702; CAA45956.1; -;
DR EMBL; AL078827; CAB44769.1; -;
DR EMBL; AL034463; CAA22429.2; -;
DR PIR; S29123; S29123.
DR HSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF001175; NAD_binding_1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 7
FT NP_BIND 153 23 POTENTIAL.
FT NP_BIND 184 184 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 306 317 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 437 448 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 535 553 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 630 646 NADP (ADP PART) (BY SIMILARITY).
SQ SEQUENCE 678 AA; 76774 MW; 6AEDDFBA6DE39C8F CRC64;

Query Match

1.5%; Score 16; DB 1; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPFRGFV 914
DB 534 IMVPGTGVAPFRGFV 549

RESULT 5
NCPR_HUMAN STANDARD; PRT; 676 AA.
AC P16435; Q16455; Q9H3M8;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN POR OR CYPOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Liver;
RX MEDLINE=90105390; PubMed=2513880;
RA Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;
RT "Structural and functional analysis of NADPH-cytochrome P-450
RT reductase from human liver: complete sequence of human enzyme and
RL NADPH-binding sites.";
RL Biochemistry 28:8639-8645(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92198003; PubMed=1550342;
RA Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
RT "Quantification of cytochrome P450 reductase gene expression in human
RT tissues.";
RL Arch. Biochem. Biophys. 294:168-172(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Czerwinski M., Sahni M., Madan A., Parkinson A.;
RT "Polymorphism of human CYPOR: expression of new allele.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Murakami H.O., Ogawa H., Nisimoto Y.;
RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase
RT in human HL-60 cell.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.
RX MEDLINE=99156068; PubMed=10048323;
RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;
RT "Crystal structure of the FMN-binding domain of human cytochrome P450
RT reductase at 1.93 Å resolution.";
RL Protein Sci. 8:298-306(1999).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- COFACTOR: FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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RT "Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and
 RL functional expression in yeast.";
 RL Blochim. Biophys. Acta 1186:137-141(1994).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferricytochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
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 CC -----
 CC EMBL; D17571; BAA04496.1; -;
 CC HSP; P00388; 1AM0.
 CC SWISS-2DPAGE; P37040; MOUSE.
 CC MGI; MGI:97744; POR.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redtase.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding; 1.
 CC Pfam; PF00258; flavodoxin; 1.
 CC Pfam; PF00687; FAD_binding; 1.
 CC PRINTS; PR00369; FLAVODOXIN.
 CC PRINTS; PR00371; FPNCR.
 CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 CC Membrane; Acetylation.
 CC INIT_MET 0 BY SIMILARITY.
 CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 CC NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 CC NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
 CC NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
 CC NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).
 CC NP_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).
 CC SEQUENCE 677 AA; 76912 MW; 0065C14D0E1C5EF8 CRC64;
 SQ
 Query Match 1.18; Score 12; DB 1; Length 677;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 899 IMVGGTGVAPF 910
 DB 528 IMVGGTGVAPF 539
 |||||
 RESULT 8
 NCPR_PIG STANDARD; PRT; 677 AA.
 AC P04175;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN POR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Amorn J., Preiss B., Stender B., Viale M., Repp R.Z., Lampert F.,
 RA Kroger M., Lumper L.;
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=87101085; PubMed=3099837;
 RX Hanlu M., Iyanagi T., Miller P., Lee T.D., Shively J.E.;
 RA "Complete amino acid sequence of NADPH-cytochrome P-450 reductase
 RT from porcine hepatic microsomes.";
 RT Biochemistry 25:7906-7911(1986).
 RN [3]
 RP SEQUENCE OF 56-677.
 RX MEDLINE=87075664; PubMed=3098240;
 RA Vogel F., Lumper L.;
 RT "Complete structure of the hydrophilic domain in the porcine NADPH-
 RT cytochrome P-450 reductase.";
 RL Biochem. J. 236:871-878(1986).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferricytochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L33893; AAA85368.1; -;
 CC PIR; A00403; RDPG04.
 CC PIR; A25584; A25584.
 CC HSP; P16435; IBIC.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redtase.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding; 1.
 CC Pfam; PF00258; flavodoxin; 1.
 CC Pfam; PF00687; FAD_binding; 1.
 CC PRINTS; PR00369; FLAVODOXIN.
 CC PRINTS; PR00371; FPNCR.
 CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 CC Membrane; Acetylation.
 CC INIT_MET 0 0
 CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 CC NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 CC NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
 CC NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
 CC NP_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).
 CC NP_BIND 623 639 NADP (ADP PART) (BY SIMILARITY).
 CC CONFLICT 54 54 S -> T (IN REF. 2).
 CC CONFLICT 163 163 T -> S (IN REF. 2).
 CC CONFLICT 174 174 N -> D (IN REF. 3).
 CC CONFLICT 339 339 T -> A (IN REF. 3).
 CC CONFLICT 378 378 N -> D (IN REF. 3).
 CC CONFLICT 400 400 Q -> E (IN REF. 3).
 CC CONFLICT 446 446 R -> L (IN REF. 2).
 CC CONFLICT 502 502 N -> D (IN REF. 3).
 CC CONFLICT 508 508 V -> L (IN REF. 2 AND 3).
 CC CONFLICT 674 674 D -> N (IN REF. 3).
 CC SEQUENCE 677 AA; 76701 MW; 26073A0B97EE3DFF CRC64;
 SQ

Query Match 1.1%; Score 12; DB 1; Length 677;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910
 DB 528 IMVPGTGVAPF 539

RESULT 9

NCPR-RABIT STANDARD; PRT; 679 AA.

AC P00389;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN POR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=87137361; PubMed=3029050;
 RA Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M.,
 RA Yamano T., Ohkawa H.;
 RT "Molecular cloning and sequence analysis of full-length cDNA for
 rabbit liver NADPH-cytochrome P-450 reductase mRNA.";
 RL J. Biochem. 100:945-954(1986).
 RN [2]
 RP PARTIAL SEQUENCE OF 1-81.
 RC TISSUE=Liver;
 RX MEDLINE=82167456; PubMed=6802823;
 RA Black S.D., Coon M.J.;
 RT "Structural features of liver microsomal NADPH-cytochrome P-450
 reductase. Hydrophobic domain, hydrophilic domain, and connecting
 region.";
 RL J. Biol. Chem. 257:5929-5938(1982).

CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 ferrocycytochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 REDUCTASE.

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CC EMBL; D00101; BAA00063.1; -
 CC EMBL; X04610; CAA28279.1; -
 CC PIR; A25505; A25505.
 CC PIR; A05233; A05233.
 CC HSSP; P16435; 1B1C.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redtse.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding.1.
 CC Pfam; PF00258; flavodoxin; 1.

DR pfam; PF00667; FAD_binding.1.
 DR PRINTS; PRO0369; FLAVODOXIN.
 DR PRINTS; PRO0371; FPNCR.
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane; Acetylation.
 FT MOD_RES 72 72
 FT NP_BIND 171 202
 FT NP_BIND 315 326
 FT NP_BIND 452 462
 FT NP_BIND 530 548
 FT NP_BIND 625 641
 FT CONFLICT 40 41
 FT CONFLICT 53 53
 FT SEQUENCE 679 AA; 76588 MW; B1A163FA53A5988B CRC64;
 E -> N (IN REF. 2).
 YW -> NY (IN REF. 2).

Query Match 1.1%; Score 12; DB 1; Length 679;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910
 DB 530 IMVPGTGVAPF 541

RESULT 10

NCPR-YEAST STANDARD; PRT; 690 AA.

AC P16603;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN NCPI OR NCPI1 OR PRD1 OR YHR042W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-12 AND 44-61.
 RX MEDLINE=89008184; PubMed=3139648;
 RA Yabusaki Y., Murakami H., Ohkawa H.;
 RT "Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450
 reductase deduced from nucleotide sequence of its cloned gene.";
 RL J. Biochem. 103:1004-1010(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 VIII.";
 RL Science 265:2077-2082(1994).

CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 ferrocycytochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 REDUCTASE.

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CC EMBL; D00101; BAA00063.1; -
 CC EMBL; X04610; CAA28279.1; -
 CC PIR; A25505; A25505.
 CC PIR; A05233; A05233.
 CC HSSP; P16435; 1B1C.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redtse.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding.1.
 CC Pfam; PF00258; flavodoxin; 1.

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CC EMBL; D13788; BAA02936.1; -;
 CC EMBL; U00062; AAB68904.1; -;
 CC PIR; A41447; A41447.
 CC PIR; S46735; S46735.
 CC HSSP; P00388; IAMO.
 CC SGB; S0001084; NCPI.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redctse.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding; 1.
 CC Pfam; PF00258; flavodoxin; 1.
 CC Pfam; PF00667; FAD_binding; 1.
 CC PRINTS; PR00369; FLAVODOXIN.
 CC PRINTS; PR00371; FPNCR.
 CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane.
 FT INIT_MET 0 0
 FT NP_BIND 148 179 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 300 311 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 435 445 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 536 554 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 638 654 NADP (ADP PART) (BY SIMILARITY).
 FT VARIANT 473 473 V -> G.
 FT CONFLICT 422 422 T -> N (IN REF. 1).
 FT SEQUENCE 690 AA; 76640 MW; FEFA18F6AB2BBD5 CRC64;

Query Match 1.1%; Score 12; DB 1; Length 690;

Best Local Similarity 100.0%; Pred. No. 0.0013; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVPFRGF 913
 |||||
 DB 539 GPGTGVPFRGF 550

RESULT 11

ID NCPR_PHAU STANDARD; PRT; 690 AA.
 AC P37116;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 OS Phaseolus aureus (Mung bean) (Vigna radiata).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucrosts 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 CC NCBI_TaxID=3916;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv Berken; TISSUE=Seedling;
 RX MEDLINE=93219390; PubMed=8464904;
 RA Shet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Estabrook R.W.;
 RT "Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894(1993).
 CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450.
 CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2 ferrocyclochrome.
 CC -!- COFACTOR: FAD AND FMN.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL

CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 CC -----
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CC EMBL; L07843; AAA34240.1; -;
 CC HSSP; P00388; IAMO.
 CC InterPro; IPR003097; FAD_binding.
 CC InterPro; IPR001709; FPN_cyt_redctse.
 CC InterPro; IPR001094; Flavodoxin_like.
 CC InterPro; IPR001226; Flavodoxin.
 CC InterPro; IPR001433; Oxred_FAD/NAD(P).
 CC Pfam; PF00175; NAD_binding; 1.
 CC Pfam; PF00258; flavodoxin; 1.
 CC Pfam; PF00667; FAD_binding; 1.
 CC PRINTS; PR00369; FLAVODOXIN.
 CC PRINTS; PR00371; FPNCR.
 CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane; Glycoprotein.
 FT NP_BIND 179 210 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 325 336 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 465 475 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 544 562 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 639 654 NADP (ADP PART) (BY SIMILARITY).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 690 AA; 76506 MW; 592966167E8561DE CRC64;

Query Match 1.0%; Score 11; DB 1; Length 690;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYYSISSSPR 836
 |||||
 DB 467 PRYYSISSSPR 477

RESULT 12

ID YB63_SCHPO STANDARD; PRT; 571 AA.
 AC Q09744;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C12C2.03c in chromosome II.
 GN SPBC12C2.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welteijns I., Vansteleers E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sapakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: SOME, TO NADPH-CYTOCHROME P450 REDUCTASES.
 CC -----
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 CC -----

DR EMBL; Z54140; CAA90816.1; -
 DR InterPro: IPR003097; FAD_binding.
 DR Pfam: PF001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00175; NAD_binding; 1.
 DR Pfam: PF00667; FAD_binding; 1.
 KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
 SQ SEQUENCE 571 AA; 6396 MW; D2EE992789307249 CRC64;

Query Match 1.0%; Score 10; DB 1; Length 571;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 906 GVAPFRGFVQ 915
 DB 405 GVAPFRGFVQ 414
 |||||

RESULT 13
 NCPR_SALTR STANDARD; PRT; 601 AA.
 AC P19618;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
 DE (Fragments).
 OS Salmo trutta (Brown trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8032;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88008061; PubMed=3116019;
 RA Urenjak J., Linder D., Lumper L.;
 RT "Structural comparison between the trout and mammalian hydrophilic
 RT domain of NADPH-cytochrome P-450 reductase.";
 RL J. Chromatogr. A 397:123-136(1987).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferrocyclochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 DR PIR: A28577; A28577.
 DR HSSP: P16435; 1B1C.
 DR InterPro: IPR001709; FPN_cyt_redctse.
 DR InterPro: IPR001094; Flavodoxin_like.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane.
 FT NON_TER 1
 FT NON_CONS 426 427
 FT NON_CONS 434 435
 SQ SEQUENCE 601 AA; 68304 MW; BC801767DEID44C9 CRC64;
 Query Match 1.0%; Score 10; DB 1; Length 601;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 EDYLOEELE 950
 DB 494 EDYLOEELE 503
 |||||

RESULT 14
 NOS1_MOUSE STANDARD; PRT; 1429 AA.
 ID NOS1_MOUSE
 AC Q92074; Q64208;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type 1) (Neuronal
 DE NOS) (N-NOS) (nNOS) (Constitutive NOS) (NC-NOS) (bNOS).
 GN NOS1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).
 RC STRAIN-BALB/C; TISSUE=Brain;
 RX MEDLINE=93312283; PubMed=7686743;
 RA Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.;
 RT "Structural-diversity of neuronal nitric oxide synthase mRNA in the nervous
 RT system.";
 RL Biochem. Biophys. Res. Commun. 193:1014-1022(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM NNOS MU).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=96212184; PubMed=8626668;
 RA Silvagno F., Xia H., Bredt D.S.;
 RT "Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform
 RT expressed in differentiated skeletal muscle.";
 RL J. Biol. Chem. 271:11204-11208(1996).
 RN [3]
 RP ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU).
 RX MEDLINE=97351924; PubMed=9208206;
 RA Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;
 RT "Regulation of neuronal nitric oxide synthase through alternative
 RT transcripts.";
 RL Dev. Neurosci. 19:224-231(1997).
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND
 CC PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A
 CC NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR
 CC THE DYSTROPHIN COMPLEX.
 CC -1- CATALYTIC ACTIVITY: L-arginine + NADPH + M O(2) = citrulline +
 CC nitric oxide + NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
 CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
 CC THE ENZYME (BY SIMILARITY).
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY
 CC N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION

OF THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED
 CC BENEATH THE SARCOLEMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING
 CC WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2,
 CC NNOS BETA, NNOS GAMMA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM;
 CC EXPRESSED IN CEREBRUM, OLFACTORY BULB, HIPPOCAMPUS, MIDBRAIN,
 CC CEREBELLUM, PONS, MEDULLA OBLONGATA, AND SPINAL CORD. ALSO FOUND
 CC IN SKELETAL MUSCLE, WHERE IT IS LOCALIZED BENEATH THE SARCOLEMA
 CC OF FAST TWITCH MUSCLE FIBERS, AND IN SPLEEN, HEART, KIDNEY, AND
 CC LIVER. N-NOS-1 AND N-NOS-2 ARE FOUND IN ALL PARTS OF THE NERVOUS
 CC SYSTEM. NNOS BETA AND GAMMA OCCUR IN A REGION-SPECIFIC MANNER IN
 CC THE BRAIN AND NNOS BETA EXPRESSION IS DEVELOPMENTALLY REGULATED.
 CC NNOS MU IS ONLY FOUND IN MATURE SKELETAL AND CARDIAC MUSCLES.
 CC -1- INDUCTION: BY CHOLINERGIC AGONISTS ACTING AT INOSITOL PHOSPHATE-
 CC LINKED MUSCARINIC RECEPTORS IN CARDIAC MYOCYTES.
 CC -1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL
 CC ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS
 CC RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES.
 CC -1- DISEASE: IN MDX MICE (MOUSE MODEL OF DYSTROPHINOPATHY) THE
 CC SARCOLEMA COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM
 CC SARCOLEMA AND ACCUMULATES IN THE CYTOSOL.
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D14552; BAA03415.1; -;
 CC EMBL: S81982; AAB36469.1; -;
 CC HSSP: P29476; IP20.
 CC MGD: MGI:97360; Nos1.
 CC InterPro: IPR003097; FAD_binding.
 CC InterPro: IPR001709; FPN_Cyt_reductase.
 CC InterPro: IPR001094; Flavodoxin_like.
 CC InterPro: IPR001226; Flavodoxin.
 CC InterPro: IPR004030; NO_synthase.
 CC InterPro: IPR001433; Oxired_FAD/NAD(P).
 CC InterPro: IPR001478; PDZ.
 CC Pfam: PF00175; NAD_binding; 1.
 CC Pfam: PF00258; flavodoxin; 1.
 CC Pfam: PF00595; PDZ; 1.
 CC Pfam: PF00667; FAD_binding; 1.
 CC Pfam: PF02898; NO_synthase; 1.
 CC PRINTS: PR00369; FLAVODOXIN.
 CC PRINTS: PR00371; PFNCR.
 CC SMART: SM00228; PDZ; 1.
 CC PROSITE: PS60001; NOS; 1.
 CC PROSITE: PS50106; PDZ; 1.
 CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
 CC Alternative splicing; Multigene family.
 CC DOMAIN 17 99
 CC DOMAIN 163 240
 CC NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
 CC SIMILARITY).
 CC HEME (BY SIMILARITY).
 CC CALMODULIN-BINDING (POTENTIAL).
 CC FMN (PYRIMIDINE PART) (BY SIMILARITY).
 CC FAD (ADP PART) (BY SIMILARITY).
 CC FAD (FLAVIN PART) (BY SIMILARITY).
 CC NADP (RIBOSE PART) (BY SIMILARITY).
 CC NADP (ADP PART) (BY SIMILARITY).
 CC MISSING (IN ISOFORM NNOS BETA).
 CC TGLQVD -> MRGLGS (IN ISOFORM NNOS BETA).
 CC MISSING (IN ISOFORM NNOS GAMMA).
 CC MISSING (IN ISOFORM N-NOS-2).
 CC 415 415
 CC 725 745
 CC 881 912
 CC 1027 1038
 CC 1170 1180
 CC 1245 1263
 CC 1343 1358
 CC 230
 CC 231 236
 CC 1 331
 CC 504 608

FT VARSPLIC 839 839 K -> KYPEPLRFFPRKGPSLSHVDSSEARSLVAARDQSHR
 FT (IN ISOFORM NNOS MU).
 SQ SEQUENCE 1429 AA; 160472 MW; 3782848D65B41BFC CRC64;
 Query Match 1.0%; Score 10; DB 1; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 826 PRYSSISSSP 835
 DQ 1172 PRYSSISSSP 1181
 RESULT 15
 NOS1_RAT
 ID NOS1_RAT STANDARD; PRT; 1429 AA.
 AC P29476; P70594;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal
 DE NOS) (N-NOS) (NNOS) (Constitutive NOS) (NC-NOS) (BNOS).
 GN NOS1 OR BNOS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91287795; PubMed=1712077;
 RA Bredt D.S., Hwang P.M., Glatt C.L., Lowenstein C., Reed R.R.,
 RA Snyder S.H.;
 RT "Cloned and expressed nitric oxide synthase structurally resembles
 RT cytochrome P-450 reductase.";
 RL Nature 351:714-718(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PNNOS).
 RC STRAIN=Fischer 344; TISSUE=Penis;
 RX MEDLINE=96400229; PubMed=8806605;
 RA Megree T., Fuentes A.M., Garban H., Rajavashisth T., Marquez D.,
 RA Rodriguez J.A., Rajfer J., Gonzalez-Cadavid N.F.;
 RT "Cloning of a novel neuronal nitric oxide synthase expressed in penis
 RT and lower urinary tract.";
 RL Biochem. Biophys. Res. Commun. 226:145-151(1996).
 RN [3]
 RP MUTAGENESIS OF TYR-588.
 RX MEDLINE=21134290; PubMed=11237702;
 RA Sato Y., Sagami I., Matsui T., Shimizu T.;
 RT "Unusual role of Tyr588 of neuronal nitric oxide synthase in
 RT controlling substrate specificity and electron transfer.";
 RL Biochem. Biophys. Res. Commun. 281:621-626(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS) OF 14-125.
 RX MEDLINE=99238815; PubMed=10221915;
 RA Hillier B.J., Christopherson K.S., Prehoda K.E., Bredt D.S., Lim W.A.;
 RT "Unexpected modes of PDZ domain scaffolding revealed by structure of
 RT nNOS-syntrophin complex.";
 RL Science 284:812-815(1999).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 963-1397.
 RX MEDLINE=21463055; PubMed=11473123;
 RA Zhang J., Martasek P., Paschke R., Shea T., Masters B.S.S.,
 RA Kim J.-J.P.;
 RT "Crystal structure of the FAD/NADPH-binding domain of rat neuronal
 RT nitric-oxide synthase. Comparisons with nadph-cytochrome p450
 RT oxidoreductase.";
 RL J. Biol. Chem. 276:37506-37513(2001).
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND
 CC PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A
 CC NEUROTRANSMITTER.
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +

nitric oxide + N NADP(+).
-1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE ENZYME (BY SIMILARITY).
-1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY
N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION
OF THE PROTEIN (BY SIMILARITY).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE. NNOS IS LOCALIZED
BENEATH THE SARCOLEMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING
WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2
AND PNNOS; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ISOFORM N-NOS1 IS EXPRESSED IN BRAIN. ISOFORM
PNNOS IS EXPRESSED IN THE PENIS, URETHRA, PROSTATE, AND SKELETAL
MUSCLE, AND COEXISTS WITH THE CEREBELLAR NNOS IN THE PELVIC
PLEXUS, BLADDER AND LIVER, AND IS DETECTABLE IN THE CEREBELLUM.
-1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL
ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS
RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES
(BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

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EMBL; X59949; CAA42574.1; -
EMBL; U67309; AAC52782.1; -
PIR; S16233; S16233
PDB; 1QAN; 06-MAR-00.
PDB; 1QAV; 06-MAR-00.
PDB; 1F20; 10-OCT-01.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR004030; NO_synthase.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR InterPro: IPR001478; PDZ.
DR Pfam; PF00175; NAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00395; PDZ; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS60001; NOS; 1.
DR PROSITE; PS50106; PDZ; 1.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW Alternative splicing; Multigene family; 3D-structure.
FT DOMAIN 17 99 PDZ.
FT DOMAIN 163 240 NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
SIMILARITY).
FT BINDING 415 415 HEME (BY SIMILARITY).
FT BINDING 588 588 CARBOXYLATE OF THE SUBSTRATE.
FT DOMAIN 725 745 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 881 912 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 1027 1038 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 1170 1180 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1245 1263 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1343 1358 NADP (ADP PART) (BY SIMILARITY).
FT VARSPLIC 504 608 MISSING (IN ISOFORM N-NOS-2).
FT VARSPLIC 839 839 K -> KYPEPLRFFPKGPSLSHVDSEAHSLVAARDSQHR
(IN ISOFORM PNNOS).
FT MUTAGEN 588 588 Y->H: 50% DECREASE OF ACTIVITY.
FT MUTAGEN 588 588 Y->S: 30% DECREASE OF ACTIVITY.

FT MUTAGEN 588 588 Y->F: NO DECREASE IN ACTIVITY.
FT CONFLICT 269 269 I -> V (IN REF. 2).
FT CONFLICT 953 953 P -> A (IN REF. 2).
FT CONFLICT 1008 1008 F -> S (IN REF. 2).
FT CONFLICT 1311 1311 A -> V (IN REF. 2).
SQ SEQUENCE 1429 AA; 160559 MW; 7255C5AE165200F5 CRC64;
Query Match 1.0%; Score 10; DB 1; Length 1429;
Best Local Similarity 100.0%; Pred.No. 0.27; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 826 PRYSSSSSP 835
DB 1172 PRYSSSSSP 1181
Search completed: May 29, 2003, 08:42:08
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:31:47 ; Search time 74 Seconds

(without alignments)
1887.117 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQPTFGELKNPLLL.....RLWLQLEEKGRYAKDVGWAG 1048

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1048	100.0	1048	22	AAB31978 Amino acid sequenc
2	1048	100.0	1048	22	B. megaterium cyto
3	1048	100.0	1048	22	B. megaterium cyto
4	1048	100.0	1049	21	AAY93566 Amino acid sequenc
5	1048	100.0	1049	22	AAB31882 Amino acid sequenc
6	961	91.7	1048	22	AAB31979 Amino acid sequenc
7	860	82.1	1048	22	AAB31980 Amino acid sequenc
8	860	82.1	1048	22	AAB31981 Amino acid sequenc
9	846	80.7	1049	22	AAV72208 Bacillus megateriu
10	266	25.4	1085	12	AA11604 P450 17-alpha/P450

11	17	1.6	17	20	AAV27545	B. megaterium p-45
12	15	1.4	693	16	AAR66738	Cytochrome-P450-ox
13	13	1.2	597	22	AAB49682	Human reductase am
14	13	1.2	700	22	AAY33673	B. bassiana pops r
15	12	1.1	677	22	AAB73901	Human derived cyto
16	12	1.1	677	22	AAB73902	Human derived cyto
17	12	1.1	678	23	ABB57261	Mouse ischaemic co
18	12	1.1	679	8	AAV70546	Sequence of rabbit
19	12	1.1	680	22	AAU27786	Human full-length
20	12	1.1	682	22	AAB82516	Rabbit NADH cytoch
21	12	1.1	685	22	AAU27958	Human contig poly
22	12	1.1	691	11	AAR05234	Sequence of yeast
23	12	1.1	1169	16	AAR76544	Mitochondrial cyto
24	10	1.0	582	22	ABB68450	Drosophila melanog
25	10	1.0	588	23	AAE20656	Helianthus tuberos
26	10	1.0	588	23	AAEL6392	Helianthus tuberos
27	10	1.0	628	22	ABG82875	S. epidermidis ope
28	10	1.0	629	23	ABP39549	Staphylococcus epi
29	10	1.0	683	20	AAW85682	Poppy cytochrome p
30	10	1.0	883	20	AAW85680	Poppy cytochrome p
31	10	1.0	1429	14	AA844489	Sequence of all or
32	10	1.0	1430	19	AAW56786	Rat neuronal nitri
33	10	1.0	1430	20	AAW28475	Rat neuronal nitri
34	10	1.0	1433	16	AAR77362	Neuronal nitrogene
35	10	1.0	1433	22	AAW31725	Amino acid sequenc
36	10	1.0	1433	22	AAW66725	Human nitric oxide
37	10	1.0	1463	18	AAW35566	Rat penile neurona
38	10	1.0	1554	20	AAW28476	Human neuronal nit
39	9	0.9	516	22	ABW58868	Drosophila melanog
40	9	0.9	516	23	AAW76367	Drosophila melanog
41	9	0.9	679	21	AAW90596	Candida tropicalis
42	9	0.9	679	21	AAW90597	Candida tropicalis
43	9	0.9	679	22	ABW64462	Drosophila melanog
44	9	0.9	679	23	ABW77082	Candida tropicalis
45	9	0.9	679	23	ABW77083	Candida tropicalis

ALIGNMENTS

RESULT 1
AAB31978
ID AAB31978 standard; Protein; 1048 AA.
XX
AC AAB31978;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a Bacillus P450 monooxygenase protein.
XX
KW Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin.
XX
OS Bacillus megaterium.
XX
PN WO200107630-A1.
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-EP07253.
XX
PR 27-JUL-1999; 99DE-1035115.
PR 18-NOV-1999; 99DE-1055605.
PR 22-MAR-2000; 2000DE-1014085.
XX
XX (BADI) BASF AG.
XX
PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
Li Q;
XX
XX WPI; 2001-182800/18.
DR N-PSDB; AAF54832.
XX
PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

especially for converting indole to indigo, has wide substrate range -
 Claim 3; Page 35-39; 54pp; German.
 The present sequence represents a cytochrome P450 monooxygenase. The
 specification describes a modified cytochrome P450 monooxygenase which
 can oxidize at least one of the following types of substrates:
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or
 CC optionally substituted cycloalkanes or cycloalkenes. The modified
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole
 CC to indigo and indorubicin. However, they may be used to oxidize many
 CC other substrates.
 XX
 SQ Sequence 1048 AA;

Query Match 100.0%; Score 1048; DB 22; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADLGEIFKFPAGRVTRYLSSORLIKE 60
 DB 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADLGEIFKFPAGRVTRYLSSORLIKE 60
 QY 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
 DB 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
 QY 121 DIAVOLVQWERLNADEHEVEPDDTRRLDITGLCGFNRYRNSFYRDPHPFITSWRA 180
 DB 121 DIAVOLVQWERLNADEHEVEPDDTRRLDITGLCGFNRYRNSFYRDPHPFITSWRA 180
 QY 181 LDEAMNKLORANPDDPAYDENKQFOEDIKVMDLVDKIIADKASGEOSDILLTHMLG 240
 DB 181 LDEAMNKLORANPDDPAYDENKQFOEDIKVMDLVDKIIADKASGEOSDILLTHMLG 240
 QY 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVNPHYLQKAAEAAARVLD 300
 DB 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVNPHYLQKAAEAAARVLD 300
 QY 301 PVPYSYQVQKLVGVHVLNEALRLWTPAFSLYAKEDVILGGEYPLEKGDDELVLIPOL 360
 DB 301 PVPYSYQVQKLVGVHVLNEALRLWTPAFSLYAKEDVILGGEYPLEKGDDELVLIPOL 360
 QY 361 HRDKTIWGDVVEFRPERFENSAIPQHAFKPGNGQACIGQOFALHEATVLVGMMLKH 420
 DB 361 HRDKTIWGDVVEFRPERFENSAIPQHAFKPGNGQACIGQOFALHEATVLVGMMLKH 420
 QY 421 FDPEDHTNVELDITKLTLPKPGFVVVYKSKKIPGLGIPSPSTEQSAKKVKKKAENHNT 480
 DB 421 FDPEDHTNVELDITKLTLPKPGFVVVYKSKKIPGLGIPSPSTEQSAKKVKKKAENHNT 480
 QY 481 PLLVLVYSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
 DB 481 PLLVLVYSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
 QY 541 PDKAFQVWLQOASADEKGVYRVSFVCGGDKNWTATYOKVPAFIDETLAAKGAENIADR 600
 DB 541 PDKAFQVWLQOASADEKGVYRVSFVCGGDKNWTATYOKVPAFIDETLAAKGAENIADR 600
 QY 601 GEADASDDPEGTYEWEHREHWSVAAVFNLDIENSEDNKSTLSLQFVDSAADWPLAKMHG 660
 DB 601 GEADASDDPEGTYEWEHREHWSVAAVFNLDIENSEDNKSTLSLQFVDSAADWPLAKMHG 660
 QY 661 AFSTNVVASKELQOQPSARSTRHELELPKESYQEGDHLGVIPRNYEIGIVNRVTFARFGL 720
 DB 661 AFSTNVVASKELQOQPSARSTRHELELPKESYQEGDHLGVIPRNYEIGIVNRVTFARFGL 720
 QY 721 DASQQLRLAEAEKLAHLPLAKTVSVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
 DB 721 DASQQLRLAEAEKLAHLPLAKTVSVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

QY 781 EALLEKQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALPISIRPRYYSISSPRVDEK 840
 DB 781 EALLEKQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALPISIRPRYYSISSPRVDEK 840
 QY 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
 DB 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
 QY 901 VGPGTGVAPFRGVQARKOLKEGOSIGLGEAHLYFGCRSPHEDYLYOELENAQSEGIITL 960
 DB 901 VGPGTGVAPFRGVQARKOLKEGOSIGLGEAHLYFGCRSPHEDYLYOELENAQSEGIITL 960
 QY 961 HTAFSRMPNQPTYYQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
 DB 961 HTAFSRMPNQPTYYQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
 QY 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048
 DB 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048

RESULT 2
 AAB46855
 ID AAB46855 standard; Protein; 1048 AA.
 XX
 AC AAB46855;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.
 XX
 KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;
 KW electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.
 XX
 OS Bacillus megaterium.
 XX
 PN W0200107573-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 27-JUL-2000; 2000WO-EP07251.
 XX
 PR 27-JUL-1999; 99DE-1035115.
 PR 10-MAR-2000; 2000DE-1011723.
 XX
 PA (BADI) BASF AG.
 XX
 PI Hauer B., Schmid RD, Schwaneberg U;
 XX
 DR WPI; 2001-159709/16.
 DR N-PSDB; AAF26268.
 XX
 PT Novel electron donor system useful for the production of
 PT omega-hydroxylated fatty acids comprises an inorganic electron sink and
 PT a mediator which enables the electron transfer -
 XX
 PS Claim 13b; Page 83-86; 94pp; German.
 XX
 CC This invention describes a novel electron donor system (M1) that
 CC transfers electrons to an enzyme with redox properties comprising an
 CC inorganic, not electrode-bound, electron sink and a mediator which enable
 CC the electron transfer. The invention also describes (1) transferring (M2)
 CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the
 CC hydrogen donor molecule is in a reaction medium comprising the oxygen
 CC transferring enzyme and (M1) in the presence of oxygen and incubating
 CC under suitable reaction conditions; (2) the enzymatic production (M3) of
 CC terminally or subterminally hydroxylated (position omega-1 to omega-4)
 CC fatty acids comprising: (i) mixing a hydroxylatable fatty acid or fatty
 CC acid derivative in the presence of (M1) and cytochrome P450
 CC monooxygenase; and (ii) isolating the hydroxylated product; (3) a
 CC bioreactor useful for the production of omega-hydroxylated fatty acids as
 CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases
 CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty

CC acid or a derivative comprising a terminal chromophore or fluorescent
CC label in (M₁); and (ii) qualitatively or quantitatively detecting the
CC signal. The invention is useful for the production of omega-hydroxylated
CC fatty acids and the detection of fatty acid monooxygenases. The
CC invention provides an alternative electron donor system of enzymes with
CC redox properties that is cheaper and more efficient, where the enzyme
CC comprises cytochrome 450.

Query Match	100.0%	Score 1048;	DB 22;	Length 1048;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1048;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	T	I	E	M	P	O	K	F	G	E	L	K	N	I	P	L	L	N	D	K	P	V	A	L	M	K	I	A	D	E	L	G	E	I	F	K	F	E	A	P	G	R	V	T	R	L	S	S	O	R	L	I	K	E	60		
Db	1	T	I	E	M	P	O	K	F	G	E	L	K	N	I	P	L	L	N	D	K	P	V	A	L	M	K	I	A	D	E	L	G	E	I	F	K	F	E	A	P	G	R	V	T	R	L	S	S	O	R	L	I	K	E	60		
Qy	61	A	C	D	E	S	R	D	K	N	L	S	O	A	L	K	F	V	R	D	F	A	G	D	G	L	T	S	W	T	H	E	K	N	W	K	A	H	N	I	L	P	S	F	S	O	A	K	M	G	Y	H	A	M	V	120		
Db	61	A	C	D	E	S	R	D	K	N	L	S	O	A	L	K	F	V	R	D	F	A	G	D	G	L	T	S	W	T	H	E	K	N	W	K	A	H	N	I	L	P	S	F	S	O	A	K	M	G	Y	H	A	M	V	120		
Qy	121	D	I	A	V	L	V	Q	K	W	E	R	L	N	A	D	H	E	I	V	E	P	D	M	T	R	L	T	D	I	G	L	C	G	F	N	Y	R	F	N	S	F	R	D	O	P	H	F	T	S	M	V	R	A	180			
Db	121	D	I	A	V	L	V	Q	K	W	E	R	L	N	A	D	H	E	I	V	E	P	D	M	T	R	L	T	D	I	G	L	C	G	F	N	Y	R	F	N	S	F	R	D	O	P	H	F	T	S	M	V	R	A	180			
Qy	181	L	D	E	A	M	N	K	L	O	R	A	N	P	D	D	P	A	Y	D	E	N	K	R	O	F	O	E	D	I	K	V	M	N	D	L	V	K	I	I	A	D	R	A	S	G	S	O	D	L	T	H	M	L	N	G	240	
Db	181	L	D	E	A	M	N	K	L	O	R	A	N	P	D	D	P	A	Y	D	E	N	K	R	O	F	O	E	D	I	K	V	M	N	D	L	V	K	I	I	A	D	R	A	S	G	S	O	D	L	T	H	M	L	N	G	240	
Qy	241	K	D	P	E	T	G	E	P	L	D	D	E	N	I	R	Y	O	I	I	T	F	L	I	A	G	H	E	T	T	S	G	L	L	S	F	A	L	Y	F	L	V	K	N	P	H	V	L	O	K	A	E	A	R	V	L	D	300
Db	241	K	D	P	E	T	G	E	P	L	D	D	E	N	I	R	Y	O	I	I	T	F	L	I	A	G	H	E	T	T	S	G	L	L	S	F	A	L	Y	F	L	V	K	N	P	H	V	L	O	K	A	E	A	R	V	L	D	300
Qy	301	P	V	S	Y	K	O	V	K	Q	L	K	Y	V	G	M	V	N	E	A	L	R	L	W	P	T	A	P	A	S	L	I	Y	A	K	E	D	T	V	L	G	G	E	P	L	E	K	G	D	E	L	A	V	I	P	O	L	360
Db	301	P	V	S	Y	K	O	V	K	Q	L	K	Y	V	G	M	V	N	E	A	L	R	L	W	P	T	A	P	A	S	L	I	Y	A	K	E	D	T	V	L	G	G	E	P	L	E	K	G	D	E	L	A	V	I	P	O	L	360
Qy	361	H	R	K	T	I	W	G	D	D	V	E	E	P	R	P	E	R	F	N	P	S	A	I	P	O	H	A	F	P	F	G	N	G	O	R	A	C	I	Q	O	F	A	L	H	E	A	T	L	V	L	G	M	L	K	H	420	
Db	361	H	R	K	T	I	W	G	D	D	V	E	E	P	R	P	E	R	F	N	P	S	A	I	P	O	H	A	F	P	F	G																										

Qy	901	VGPGTVAPPRGFVQARQKQLKEQGQSIGEAHLIFGCGRSPHEDYLYQELENAAQSEGIITL	960
Dd	901	VGPGTVAPPRGFVQARQKQLKEQGQSIGEAHLIFGCGRSPHEDYLYQELENAAQSEGIITL	960
Qy	961	HTAFSRMPNPQPTVVQHVMEDQDGKKLELLDQGAHFHYICGDGSOMAPAVEATLMKSADV	1020
Dd	961	HTAFSRMPNPQPTVVQHVMEDQDGKKLELLDQGAHFHYICGDGSOMAPAVEATLMKSADV	1020
Qy	1021	HQVSEADARLWLOOLEEKGRYAKDVWAG	1048
Dd	1021	HQVSEADARLWLOOLEEKGRYAKDVWAG	1048
 RESULT 3 AAB46856 ID AAB46856 standard; Protein; 1048 AA. XX XX AAB46856; XX DT 02-MAY-2001 (first entry) XX DE DE B. megaterium cytochrome P450 monooxygenase BM-3 protein. KW KW Cytochrome P450 monooxygenase; BM-3; site-specific mutagenesis; KW KW aliphatic carboxylic acid hydroxylation; fatty acid. XX OS Bacillus megaterium. XX XX WO200107574-A2. XX XX 01-FEB-2001. XX 27-JUL-2000; 2000WO-EP07252. XX PF 27-JUL-1999; 99DE-1035115. XX PR 10-MAR-2000; 2000DE-1011723. XX XX PA (BADI) BASF AG. XX XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R; PI LI Q; XX XX WPI: 2001-159710/16. DR N-PSDB; AAF26324. XX XX PT New modified cytochrome P450 mono-oxygenase, useful for producing PT PT hydroxylated aliphatic carboxylic acids and derivatives, has altered PT PT substrate specificity - XX XX Claim 3; Page 41-45; 49pp; German. PS XX This invention describes a novel modified cytochrome P450 (I) having, as CC CC a result of site-specific mutagenesis of its substrate-binding domain, CC CC an altered substrate profile, relative to the wild-type, when used for CC CC terminal and/or subterminal enzymatic hydroxylation of aliphatic CC CC carboxylic acids. The invention also describes (1) nucleic acid (II) CC CC encoding (I), and its complement; (2) expression cassette (EC) containing CC CC (II) and control elements; (3) a vector containing at least one EC; (4) CC CC recombinant microorganisms transformed with at least one vector of (3); CC CC and (5) enzymatic production of terminally and/or subterminally CC CC hydroxylated aliphatic carboxylic acids (A) using the microorganisms of CC CC (4), or isolated (I). (I), and recombinant cells that express them, are CC CC used to produce hydroxylated aliphatic carboxylic acids or their CC CC derivatives (esters and amides). (I) have altered substrate specificity, CC CC especially for hydroxylation of 8-12C fatty acids at the omega-1, -2 CC CC and/or -3 positions, and may also have increased reactivity and/or CC CC regioselectivity. XX XX Sequence 1048 AA; SQ			

Query Match	100.0%;	Score 1048;	DB 22;	Length 1048;
Best Local Similarity	100.0%;	Pred. No. 0;		

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TIKEMPQKTFGELKPLNLTNDKPVQALMKTADELGEIFKFEAPGRVTRVYSSQRLIKE	60
Db	1	TIKEMPQKTFGELKPLNLTNDKPVQALMKTADELGEIFKFEAPGRVTRVYSSQRLIKE	60
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
Db	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
QY	121	DIAVQLVKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSMVRA	180
Db	121	DIAVQLVKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSMVRA	180
QY	181	LDEAMNKLORANPDPAIDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG	240
Db	181	LDEAMNKLORANPDPAIDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG	240
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEFAARVLVD	300
Db	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEFAARVLVD	300
QY	301	PVPSTKQVKQLYVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL	360
Db	301	PVPSTKQVKQLYVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL	360
QY	361	HRDKTIWGDVVEEFPERENPNSAIPQHAFFKFGNGORACIGQOFALHEATLVIGMLKH	420
Db	361	HRDKTIWGDVVEEFPERENPNSAIPQHAFFKFGNGORACIGQOFALHEATLVIGMLKH	420
QY	421	FPFEDHNTYELDIKETLTLKPGFVYVKAASKKIPIGGIPSPSTEQSAKKVKKKAENAHNT	480
Db	421	FPFEDHNTYELDIKETLTLKPGFVYVKAASKKIPIGGIPSPSTEQSAKKVKKKAENAHNT	480
QY	481	PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDHSHAGNLPREGAVLIYTSYNGHP	540
Db	481	PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDHSHAGNLPREGAVLIYTSYNGHP	540
QY	541	PONAKQFVMDLQASADEVKGVYSVFGGDKNMTATYQKVPFIDETLAAGAENIADR	600
Db	541	PONAKQFVMDLQASADEVKGVYSVFGGDKNMTATYQKVPFIDETLAAGAENIADR	600
QY	601	GEADASDDPEGTYEWRHNMWSDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660
Db	601	GEADASDDPEGTYEWRHNMWSDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660
QY	661	AFSTNVVSKELQOPCSARSTRHLELPEKASVQEGDHLGVIIPRYEGIVNRVTARFGL	720
Db	661	AFSTNVVSKELQOPCSARSTRHLELPEKASVQEGDHLGVIIPRYEGIVNRVTARFGL	720
QY	721	DASQIIRLEAEELKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPKHVEL	780
Db	721	DASQIIRLEAEELKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPKHVEL	780
QY	781	EALKEQAYKEOVLAKRLTMELEKYPACENKMFSEFIALPLSIRPRYISSSSPRVDEK	840
Db	781	EALKEQAYKEOVLAKRLTMELEKYPACENKMFSEFIALPLSIRPRYISSSSPRVDEK	840
QY	841	QASITVSVVSGAWSGYEGYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	900
Db	841	QASITVSVVSGAWSGYEGYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	900
QY	901	VGPFGTVAPFRGVQARQLKEQOSGLGEAHLVFCRSPHEDYLYQEELENAQSGIITL	960
Db	901	VGPFGTVAPFRGVQARQLKEQOSGLGEAHLVFCRSPHEDYLYQEELENAQSGIITL	960
QY	961	HTAFSRMPNQPTYYVQHVEQDGKKLIELLDQGAHFYICGGGQSMAPAVEATLMKSYADV	1020
Db	961	HTAFSRMPNQPTYYVQHVEQDGKKLIELLDQGAHFYICGGGQSMAPAVEATLMKSYADV	1020
QY	1021	HOVSADARLWTLQLEEKGRYAKDVWAG	1048
Db	1021	HOVSADARLWTLQLEEKGRYAKDVWAG	1048

RESULT 4	
AA93566	
ID	AA93566 standard; Protein; 1049 AA.
XX	
AC	AA93566;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of the P450-BM3 sequence.
XX	
KW	Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;
KW	infection; P450-BM3.
XX	
OS	Unidentified.
XX	
FH	Key
FT	Misc-difference 303.
FT	/note= "Val encoded by GCT"
FT	Misc-difference 471
FT	/note= "Val encoded by GCA"
XX	
PN	WO200031273-A2.
XX	
PD	02-JUN-2000.
XX	
PD	19-NOV-1999; 99WO-GB03873.
XX	
PR	19-NOV-1998; 98GB-0025421.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
XX	
PI	Wong LL, Bell SG, Carmichael AB;
XX	
DR	WPI; 2000-451679/39.
DR	N-PSDB; AAA46648.
XX	
PT	Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or
PT	derivatives for preventing or treating infection in human or animal
PT	body comprises mutant haem-containing enzyme which has substitution of
PT	amino acid in the active site -
XX	
PS	Disclosure; Page 51-53; 63pp; English.
XX	
CC	The specification describes a process for oxidizing an acyclic or
CC	cyclic terpene, a cycloalkene, or a derivative. The process comprises
CC	oxidizing the compound with a mutant haem-containing enzyme which
CC	comprises a substitution of an amino acid in the active site by an
CC	amino acid with a less polar side-chain. The process is useful for
CC	oxidizing an acyclic or cyclic terpene, a cycloalkene, or their
CC	derivatives. The process is also useful for producing an oxidation
CC	product useful for preventing or treating infection in a human or
CC	animal body. The present sequence represents the amino acid sequence of
CC	the P450-BM3 sequence. The protein is used to construct enzymes
CC	for use in the process of the invention.
XX	
SQ	Sequence 1049 AA;
Query Match	100.0%; Score 1048; DB 21; Length 1049;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TIKEMPQKTFGELKPLNLTNDKPVQALMKTADELGEIFKFEAPGRVTRVYSSQRLIKE 60
Db	2 TIKEMPQKTFGELKPLNLTNDKPVQALMKTADELGEIFKFEAPGRVTRVYSSQRLIKE 61
QY	61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120
Db	62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121
QY	121 DIAVOLVKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSMVRA 180

Db 422 DFDHNTNYELDKETLTLPKPGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHNT 481
 QY 481 PLLVLYGSMGTAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540
 Db 482 PLLVLYGSMGTAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 541
 QY 541 PDNAKQFVDWLQDASADEVKGVYRVFGCGDKNWTYQKVPFIDETLAAGAENIADR 600
 Db 542 PDNAKQFVDWLQDASADEVKGVYRVFGCGDKNWTYQKVPFIDETLAAGAENIADR 601
 QY 601 GADASDDPEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 660
 Db 602 GADASDDPEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 661
 QY 661 AFSTNVASKELQPGSARSTRHLELPEKASVQGDHGLVIPRNYEGIVNRVTAREGL 720
 Db 662 AFSTNVASKELQPGSARSTRHLELPEKASVQGDHGLVIPRNYEGIVNRVTAREGL 721
 QY 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
 Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
 QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFTALLPSIRPRYISISSPRVDEK 840
 Db 782 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFTALLPSIRPRYISISSPRVDEK 841
 QY 841 QASITVSVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM 900
 Db 842 QASITVSVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM 901
 QY 901 VGPFGTVAPFRGVQARKQKQSGSLGEAHLVFCRSPHEDYLYQEELENAQSGEITL 960
 Db 902 VGPFGTVAPFRGVQARKQKQSGSLGEAHLVFCRSPHEDYLYQEELENAQSGEITL 961
 QY 961 HTAFSRMPNPQTYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
 Db 962 HTAFSRMPNPQTYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
 QY 1021 HOVSADARLWQLLEEKGRYAKDVWAG 1048
 Db 1022 HOVSADARLWQLLEEKGRYAKDVWAG 1049

RESULT 6
 AAB31979
 ID AAB31979 standard; Protein; 1048 AA.
 XX
 AC AAB31979;
 DT 15-MAY-2001 (first entry)
 XX
 DE Amino acid sequence of a modified P450 monooxygenase protein.
 XX
 KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
 XX
 OS Bacillus megaterium.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 87
 FT /note= "wild type Phe changed to Val"
 XX
 PN WO200107630-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 27-JUL-2000; 2000WO-EP07253.
 XX
 PR 27-JUL-1999; 99DE-1035115.
 PR 18-NOV-1999; 99DE-1055605.
 PR 22-MAR-2000; 2000DE-1014085.
 XX
 PA (BADI) BASF AG.
 XX

PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
 LI Q;
 XX
 DR WPI; 2001-182800/18.
 XX
 PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
 especially for converting indole to indigo, has wide substrate range
 XX
 PS Claim 5; Page -; 54pp; German.
 XX
 CC The present sequence represents a modified cytochrome P450 monooxygenase.
 The specification describes a modified cytochrome P450 monooxygenase
 which can oxidize at least one of the following types of substrates:
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
 poly-cyclic aromatics; linear or branched alkanes or alkenes; or
 CC optionally substituted cycloalkanes or cycloalkenes. The modified
 cytochrome P450 monooxygenase are specifically used to oxidize indole
 to indigo and indorubicin. However, they may be used to oxidise many
 CC other substrates.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 XX
 SQ Sequence 1048 AA;
 Query Match 91.7%; Score 961; DB 22; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 961; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 88 TSWTEKNWKAHNILLPSFQQAMKGYHAMVDIAVOLVKWERLNADHEIEVEDMTR 147
 Db 88 TSWTEKNWKAHNILLPSFQQAMKGYHAMVDIAVOLVKWERLNADHEIEVEDMTR 147
 QY 148 LTLDITIGLCGNYRNSFYRQDPHPFITSMVRALDEAMNKLRANPDPAIDENKROQE 207
 Db 148 LTLDITIGLCGNYRNSFYRQDPHPFITSMVRALDEAMNKLRANPDPAIDENKROQE 207
 QY 208 DIKVNNDLVDKIADRKASGSDLLTHMLNGKDPETGEPLDDENIRYQITITFLIAGHE 267
 Db 208 DIKVNNDLVDKIADRKASGSDLLTHMLNGKDPETGEPLDDENIRYQITITFLIAGHE 267
 QY 268 TTSGLLSFALYFLVKNPHVLOKAAEAAARLVDPVPSYKQVKQLKYGVMVNEALRLMPT 327
 Db 268 TTSGLLSFALYFLVKNPHVLOKAAEAAARLVDPVPSYKQVKQLKYGVMVNEALRLMPT 327
 QY 328 APFSLYAKEDTVLGGEYPLEKDELMLVLIIPOLHRDKTIGWDVDEEFPERFENPSAIPQ 387
 Db 328 APFSLYAKEDTVLGGEYPLEKDELMLVLIIPOLHRDKTIGWDVDEEFPERFENPSAIPQ 387
 QY 388 HAFKPFNGQACIGQQFALHEATLVLCGMLKHFDEFDHTNYELDIKETLTLPKPGFVVK 447
 Db 388 HAFKPFNGQACIGQQFALHEATLVLCGMLKHFDEFDHTNYELDIKETLTLPKPGFVVK 447
 QY 448 AKSKKIPGLGIPSPSTEQSAKKVRKAENAHNTPLLVLYGSMGTAGTARDLADIAKSK 507
 Db 448 AKSKKIPGLGIPSPSTEQSAKKVRKAENAHNTPLLVLYGSMGTAGTARDLADIAKSK 507
 QY 508 GFAPQVATLDSHAGNLPREGAVLIIVTASNGHPPDNKQFVDWLQDASADEVKGVYRVSVF 567
 Db 508 GFAPQVATLDSHAGNLPREGAVLIIVTASNGHPPDNKQFVDWLQDASADEVKGVYRVSVF 567
 QY 568 CGCDKNWATTYQKVPFIDETLAAGAENIADRGEADASDDFEGTYEWRHMSDVAAY 627
 Db 568 CGCDKNWATTYQKVPFIDETLAAGAENIADRGEADASDDFEGTYEWRHMSDVAAY 627
 QY 628 FNLDIENSEDNKSTLSLQFVDSADMPKAKMHGAFSTNVVASKELQPGSARSTRHLEIE 687
 Db 628 FNLDIENSEDNKSTLSLQFVDSADMPKAKMHGAFSTNVVASKELQPGSARSTRHLEIE 687
 QY 688 LPKEASYOEGDHLGVIPRNYEGIVNRVTAREGLDASQOIRLEAEEKLAHLPLAKTVSVE 747
 Db 688 LPKEASYOEGDHLGVIPRNYEGIVNRVTAREGLDASQOIRLEAEEKLAHLPLAKTVSVE 747

QY 748 ELLQYVELQDPVTRTQLRAMAATVCPPHKVELEALLEKQAYKEQVLAKRLTLMLELEKY 807
 Db |||||||
 QY 808 PACEMKSEFIALPSIRPRYSISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNY 867
 Db |||||||
 QY 868 LAELQEGDITCFISIPQSEFTLPKDPETPLIMVGCTGVAPRFGFQARKQLKEQGQSL 927
 Db |||||||
 QY 928 GEALYFGCRSPHEDYLYOELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKKLI 987
 Db |||||||
 QY 988 ELLDQGAHFYICGDSQMAPAVEATLMKSYADVHVQVSEADARLWLOOLEEKGRYAKDVA 1047
 Db |||||||
 QY 1048 G 1048
 Db |||||||
 RESULT 7
 AAB31980
 ID AAB31980 standard; Protein; 1048 AA.
 AC AAB31980;
 DT 15-MAY-2001 (first entry)
 XX
 DE Amino acid sequence of a modified P450 monooxygenase protein.
 XX
 KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
 XX
 OS Bacillus megaterium.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 87
 FT Misc-difference /note= "wild type Phe changed to Val"
 FT Misc-difference 188
 FT Misc-difference /note= "wild type Leu changed to Gln"
 XX
 PN W0200107630-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 27-JUL-2000; 2000WO-EP07253.
 XX
 PR 27-JUL-1999; 99DE-1035115.
 PR 18-NOV-1999; 99DE-1055605.
 PR 22-MAR-2000; 2000DE-1014085.
 XX
 PA (BADI) BASF AG.
 XX
 PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
 PI Li Q;
 XX
 DR WPI; 2001-182800/18.
 XX
 PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
 PT especially for converting indole to indigo, has wide substrate range -
 XX
 PS Claim 5; Page -: 54pp; German.
 XX
 CC The present sequence represents a modified cytochrome P450 monooxygenase.
 CC The specification describes a modified cytochrome P450 monooxygenase
 CC which can oxidize at least one of the following types of substrates:
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or

CC optionally substituted cycloalkanes or cycloalkenes. The modified
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole
 CC to indigo and indorubicin. However, they may be used to oxidise many
 CC other substrates.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 XX
 SQ Sequence 1048 AA;
 Query Match 82.1%; Score 860; DB 22; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 189 QRANPDPPAYDENKROFQEDIKYMNDLVKIIADRKASGEQSDLLTHMLNGKDPETGE 248
 Db |||||||
 QY 249 LDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDPVPSYKQV 308
 Db |||||||
 QY 309 KOLKYVGMVLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQLHRDKTIWG 368
 Db |||||||
 QY 369 DYVEEFPERFENPSAIPQAHAFKPFNGQACIQQFALHEATLVGLMMLKHDFEDHTN 428
 Db |||||||
 QY 429 YELDIKETLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHNTPLLVIYGS 488
 Db |||||||
 QY 489 NMCTAECTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFV 548
 Db |||||||
 QY 549 DWLDQASADEVKGVYSVFGCGDKNWTYYQKPAFIDETLAAGAENIADRGADASDD 608
 Db |||||||
 QY 609 FEGTYEWRHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKHGAFTNVA 668
 Db |||||||
 QY 669 SKELQOPGSARSTRHLEIELPKEASYOEGDHLGVIPRNYEGIVNRVTARGLDASQIQL 728
 Db |||||||
 QY 729 EABEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVELEALLEKQA 788
 Db |||||||
 QY 789 YKEQVLAKRLTLMLELEKYPACEMKSEFIALPSIRPRYSISSSPRDEKQASITVSV 848
 Db |||||||
 QY 849 VSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIMVGGTGA 908
 Db |||||||
 QY 909 PFRGFGVQARKQLKEQGSLGEAHLVFCRSPHEDYLYOELENAQSEGIITLHTAFSRMP 968
 Db |||||||
 QY 969 NQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADVHVQVSEAD 1028
 Db |||||||
 QY 1029 RLWLOOLEEKGRYAKDVAWAG 1048
 Db |||||||
 QY 1029 RLWLOOLEEKGRYAKDVAWAG 1048

CC containing the recombinant sequence encoding the fusion protein, is
CC used to transform *Saccharomyces cerevisiae*. The transformant is
CC designated AH22(p(alphaBM-1)) and can be used for the synthesis of
CC steroids.

XX
SQ Sequence 1085 AA;
Query Match 25.4%; Score 266; DB 12; Length 1085;
Best Local Similarity 100.0%; Pred. No. 5.9e-260;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 768 AAKTVCPPHKVEALELLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRP 827
DB 806 AAKTVCPPHKVEALELLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRP 865
QY 828 YSISSSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITCFISTPQSE 887
DB 866 YSISSSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITCFISTPQSE 925
QY 888 FTLPKDPETPLIMVGPGTGVAPFRGFVQARKQKQGSIGEAHLYFGCRSPHEDYLYQE 947
DB 926 FTLPKDPETPLIMVGPGTGVAPFRGFVQARKQKQGSIGEAHLYFGCRSPHEDYLYQE 985
QY 948 ELENQSGEIIITHTAFSRMPNPKTYVOHVMEQDGKKLIELLDQGAHYICGDSQMAP 1007
DB 986 ELENQSGEIIITHTAFSRMPNPKTYVOHVMEQDGKKLIELLDQGAHYICGDSQMAP 1045
QY 1008 AVENTLMKSYADVHVQVSEADARLWLQ 1033
DB 1046 AVENTLMKSYADVHVQVSEADARLWLQ 1071

RESULT 11
AAV27545
ID AAY27545 standard; peptide; 17 AA.
XX
AC AAY27545;
DT 30-NOV-1999 (first entry)
XX
DE B. megaterium P-450BM-3 peptide fragment.
XX
KW Monoamine Oxidase; MAO; mutation; MAO B; cellular neurotransmitter;
KW vasoamine; enzyme; human; P-450.
XX
OS Bacillus megaterium.
XX
PN W09946297-A1.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US05173.
XX
PR 11-MAR-1998; 98US-0077482.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Abell CW, Lewis DA;
XX
DR WPI; 1999-561665/47.
XX

PT New mutant enzyme useful for regulation of neurotransmitters -
PS
PS Example 1; Fig 1; 37pp; English.
XX
XX The invention provides an isolated, mutated Monoamine Oxidase B (MAO B)
CC enzyme having at least one amino acid substitution for wild-type amino
CC acids in a MAO B active site, the wild-type amino acid residues selected
CC from Phe423, Glu427 and Thr428. A plasmid containing the DNA encoding the
CC mutated MAO B and regulatory elements can be used for the recombinant
CC expression of the enzyme. The mutated MAO B enzyme is useful for indirect
CC regulation of cellular neurotransmitters and vasoamines, as the
CC substitutions reduce MAO B's activity and alters its pH profile. The

CC present sequence represents a B. megaterium P-450BM-3 peptide fragment.
XX
SQ Sequence 17 AA;

Query Match 1.6%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 259 ITFLIAGHETTSGLLSF 275
DB 1 ITFLIAGHETTSGLLSF 17

RESULT 12
AAR66738
ID AAR66738 standard; Protein; 693 AA.
XX
AC AAR66738;
DT 19-JUL-1995 (first entry)
XX
DE Cytochrome-P450-oxidoreductase.
XX
KW Cytochrome-P450-oxidoreductase; monooxygenase.
XX
OS Aspergillus niger ATCC 1015.
XX
PN W09429453-A.
XX
PD 22-DEC-1994.
XX
PF 10-JUN-1994; 94WO-NL00135.
XX
PR 11-JUN-1993; 93NL-0001025.
XX
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
XX
PI Van DEN BRINK JM, Van GORCOM RF, Van GORCOM RFM;
XX
DR WPI; 1995-036481/05.
XX
DR N-PSDB; AAO79914.
XX

PT Recombinant DNA mol. encoding cytochrome P450 oxidoreductase -
PT esp. isolated from filamentous fungi, useful for increasing
PT monooxygenase enzymatic conversion
XX
PS Disclosure; Fig. 2; 46pp; English.
XX

CC The primers given in AAQ79915-19 were used for the PCR amplification
CC of A. niger ATCC 1015 chromosomal DNA. These degenerate primers are
CC based on conserved sequences in known cytochrome-P450-
CC oxidoreductases. The DNA sequence of an isolated clone, given in
CC AAQ79914, encodes a cytochrome-P450-oxidoreductase having the
CC sequence given in AAR66738.

XX
SQ Sequence 693 AA;
Query Match 1.4%; Score 15; DB 16; Length 693;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 899 IMVGPGTGVAPFRGF 913
DB 544 IMVGPGTGVAPFRGF 558

RESULT 13
AAB49682
ID AAB49682 standard; Protein; 597 AA.
XX
AC AAB49682;
XX
DT 03-APR-2001 (first entry)

XX DE Human reductase amino acid sequence.
 XX KW Human; reductase; flavoprotein; cytochrome p450 reductase; chromosome 9;
 XX KW nitric oxide synthase; cancer; drug bioactivation.
 XX OS Homo sapiens.
 XX PN WO200077180-A1.
 XX PD 21-DEC-2000.
 XX PF 13-JUN-2000; 2000WO-US16245.
 XX PR 16-JUN-1999; 99US-0334490.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PI Powell DJ, Tew DG;
 XX DR WPI: 2001-112221/12.
 XX DR N-PSDB; AAF29129.
 XX PT New isolated reductase polypeptides and polynucleotides, useful in
 XX PT screening assays, particularly for diagnosing a disease associated with
 XX PT altered levels of reductase and as vaccines to protect an individual
 XX PT against these diseases -
 XX PS Claim 1; Page 25-26; 27pp; English.
 XX CC The present invention relates to DNA sequence AAF29129 which encodes a
 XX CC human reductase represented in AAB49682. The DNA sequence shows homology
 XX CC with nucleotide sequences of cytochrome p450 reductases and nitric oxide
 XX CC synthases. The protein is related to members of the FNR family of
 XX CC flavoproteins. This reductase gene maps to human chromosome 9. The
 XX CC reductase polypeptide and polynucleotide are useful in screening assays,
 XX CC particularly as diagnostic reagents for detecting abnormally decreased or
 XX CC increased levels of the reductase polypeptide or mRNA expression. In
 XX CC particular, these are useful for diagnosing or determining susceptibility
 XX CC of a subject to a disease associated with altered levels of reductase
 XX CC polypeptide. Diseases which may be treated by methods using the reductase
 XX CC include cancer, and the sequences may be used in methods for drug
 XX CC bioactivation. The polypeptides and polynucleotides may also be used as
 XX CC vaccines to protect an individual against these diseases. The polypeptide
 XX CC or its fragments are also useful as immunogens to produce antibodies that
 XX CC are immunospecific for the reductase polypeptides. The polynucleotide
 XX CC sequences may also be used in chromosome localization studies and tissue
 XX CC expression studies.
 XX SQ Sequence 597 AA;
 Query Match 1.28; Score 13; DB 22; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 899 IMVGPGRGVAPFR 911
 Db 454 IMVGPGRGVAPFR 466
 RESULT 14
 AAY33673
 ID AAY33673 standard; Protein; 700 AA.
 XX AC AAY33673;
 XX DT 07-JAN-2000 (first entry)
 XX DE B. bassiana POPS reductase protein.
 XX KW POPS; 2-phenoxypolipionic acid; 2-(4-hydroxyphenoxo) propionic acid;
 XX KW herbicide intermediate; hydroxylation rate; reductase.

OS Beauveria bassiana.
 XX PN DE19814528-A1.
 XX PD 07-OCT-1999.
 XX PF 01-APR-1998; 98DE-1014528.
 XX PR 01-APR-1998; 98DE-1014528.
 XX PA (BADI) BASF AG.
 XX PI Hauer B, Dingler C, Van Gorcom R, Van Zeljl C;
 XX DR WPI: 1999-552253/47.
 XX DR N-PSDB; AA23663.
 XX PT Production of 2-(4-hydroxyphenoxo) propionic acid from
 XX PT 2-phenoxypolipionic acid using microorganism having increased
 XX PT hydroxylation rate -
 XX PS Example 5; Page 28-31; 36pp; German.
 XX CC This invention describes a novel method for the production of
 XX CC 2-(4-hydroxyphenoxo) propionic acid (I) from 2-phenoxypolipionic acid
 XX CC (POPS) or its salts. The method comprises a microorganism containing at
 XX CC least one of the genes contained within a Beauveria bassiana genomic
 XX CC sequence of 11292 bp (I), with two open reading frames. (I) is useful
 XX CC as a herbicide intermediate. Microorganisms containing multiple copies of
 XX CC (I) have significantly increased hydroxylation rates. This sequence
 XX CC represents the Beauveria bassiana POPS reductase described in the method
 XX CC of the invention.
 XX SQ Sequence 700 AA;
 Query Match 1.28; Score 13; DB 20; Length 700;
 Best Local Similarity 100.0%; Pred. No. 0.00093;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 899 IMVGPGRGVAPFR 911
 Db 541 IMVGPGRGVAPFR 553
 RESULT 15
 AAB73901
 ID AAB73901 standard; Protein; 677 AA.
 XX AC AAB73901;
 XX DT 22-MAY-2001 (first entry)
 XX DE Human derived cytochrome p450 reductase.
 XX KW Human; cytochrome p450 monooxygenase; cytochrome p450 reductase; NPR;
 XX KW pigment production; indole; dye; cosmetic industry; marker.
 XX OS Homo sapiens.
 XX PN WO200114565-A1.
 XX PD 01-MAR-2001.
 XX PF 11-AUG-2000; 2000WO-AU00966.
 XX PR 11-AUG-1999; 99AU-0002156.
 XX PA (UYOU) UNIV QUEENSLAND.
 XX PA (UYVA-) UNIV VANDERBILT.
 XX PA (CALI) CALIFORNIA INST OF TECHNOLOGY.
 XX PI Gillam EJ, Notley LM, Devoss J, Guengerich FP, Volkov A;
 XX XX

DR WPI; 2001-257635/26.
 DR N-PSDB; AAF76960.
 XX Generation of genetically modified cell to produce pigment -
 PT
 XX
 PS Claim 39; Page 145-148; 178pp; English.
 XX
 CC The present sequence is cytochrome P450 reductase. The invention
 CC relates to a method for producing pigment using cells containing
 CC cytochrome P450 sequences. It involves the use of genetic material
 CC encoding a cytochrome P450 protein or a functional derivative or
 CC homologue of it in the generation of a genetically modified cell. The
 CC cell has the capacity to produce a pigment in the presence of indole,
 CC or a precursor, analogue or derivative of indole, upon expression of
 CC the genetic material. Pigment from plant or plant material is useful
 CC in the dye or cosmetic industry or as commercial tags or as markers for
 CC transformation of microbial, plant or animal cells.
 XX
 SQ Sequence 677 AA;
 Query Match 1.1%; Score 12; DB 22; Length 677;
 Best Local Similarity 100.0%; Pred. No. 0.0093;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 899 IMVPGGTGVAPF 910
 Db 529 IMVPGGTGVAPF 540
 |||||

Search completed: May 29, 2003, 08:41:38
 Job time : 78 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:27:11 ; Search time 29 Seconds
(without alignments)
1063.284 Million cell updates/sec

Title: US-10-031-146-2
Perfect score: 1048
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	1.9	20	4	US-09-057-897-30
2	17	1.6	17	4	US-09-265-653-20
3	15	1.4	693	1	US-08-553-279-2
4	10	1.0	588	4	US-09-627-216A-14
5	10	1.0	629	4	US-09-134-001C-4394
6	10	1.0	1429	1	US-07-642-002-2
7	10	1.0	1429	2	US-08-365-486A-13
8	10	1.0	1429	2	US-08-319-866-11
9	10	1.0	1429	4	US-08-880-342-13
10	10	1.0	1430	2	US-08-705-625-4
11	10	1.0	1430	3	US-09-010-998-5
12	10	1.0	1430	4	US-09-220-574-4
13	10	1.0	1433	2	US-08-365-486A-21
14	10	1.0	1433	4	US-09-123-708-4
15	10	1.0	1433	4	US-09-123-624-4
16	10	1.0	1433	4	US-08-880-342-21
17	10	1.0	1434	2	US-08-365-486A-19
18	10	1.0	1434	4	US-08-880-342-19
19	10	1.0	1554	2	US-08-705-625-3
20	10	1.0	1554	3	US-09-010-998-6
21	10	1.0	1554	4	US-09-220-574-3
22	9	0.9	679	4	US-09-302-620B-83
23	9	0.9	679	4	US-09-302-620B-84
24	9	0.9	1144	1	US-08-147-812-5
25	9	0.9	1144	2	US-08-319-866-12
26	9	0.9	1144	4	US-09-123-708-2
27	9	0.9	1144	4	US-09-123-624-2

28 8 0.8 406 6 5212296-6
29 8 0.8 412 1 US-08-102-863-11
30 8 0.8 412 1 PCT-US92-10885-11
31 8 0.8 504 1 US-08-457-274A-25
32 8 0.8 504 5 PCT-US95-05758-25
33 8 0.8 505 4 US-09-627-216A-12
34 8 0.8 505 4 US-09-126-420A-22
35 8 0.8 513 4 US-09-351-229-4
36 8 0.8 576 3 US-08-948-564-16
37 8 0.8 1350 2 US-08-319-866-9
38 7 0.7 29 4 US-09-082-358B-34
39 7 0.7 33 2 US-08-511-872-4
40 7 0.7 33 2 US-08-511-872-6
41 7 0.7 33 2 US-08-511-872-9
42 7 0.7 33 2 US-08-511-872-10
43 7 0.7 33 2 US-08-511-872-11
44 7 0.7 103 3 US-08-894-173-77
45 7 0.7 103 4 US-09-398-193-77

ALIGNMENTS

RESULT 1
US-09-057-897-30
; Sequence 30, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cytochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-057-897-30

Query Match 1.9%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 VDKIIADRKASGQSDLLT 235
Db 1 VDKIIADRKASGQSDLLT 20

RESULT 2

US-09-265-653-20
; Sequence 20, Application US/09265653
; Patent No. 6451570
; GENERAL INFORMATION:
; APPLICANT: Abeil, Creed W.
; APPLICANT: Lewis, Duane A.
; TITLE OF INVENTION: Mutants of Monoamine Oxidase B
; FILE REFERENCE: D6048
; CURRENT APPLICATION NUMBER: US/09/265,653
; CURRENT FILING DATE: 1999-03-10
; EARLIER APPLICATION NUMBER: US 60/077,482
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; FEATURE:
; OTHER INFORMATION: Amino acid sequence containing conserved site of
; OTHER INFORMATION: Bacillus megaterium P-450BM3
US-09-265-653-20

Query Match 1.6%; Score 17; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 ITFLIAGHETTSGLLSF 275
Db 1 ITFLIAGHETTSGLLSF 17
|||||

RESULT 3

US-08-553-279-2
; Sequence 2, Application US/08553279
; Patent No. 5801024
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 5801024el oxidoreductase from filamentous funghi,
; TITLE OF INVENTION: DNA coding therefore and cells transformed with said DNA.
; NUMBER OF SEQUENCES: 9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,279
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP PCT/NL94/00135
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 693 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-553-279-2

Query Match 1.4%; Score 15; DB 1; Length 693;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVGPCTGVAPRGRF 913
Db 544 INVGPCTGVAPRGRF 558
|||||

RESULT 4

US-09-627-216A-14
; Sequence 14, Application US/09627216A
; Patent No. 6368837
; GENERAL INFORMATION:
; APPLICANT: Sariaslani, Sima F
; APPLICANT: Tang, Xiao-Song
; APPLICANT: Qi, Wei Wei
; APPLICANT: Vannelli, Todd
; APPLICANT: Gatenby, Anthony
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
; FILE REFERENCE: BC1009 US NA
; CURRENT APPLICATION NUMBER: US/09/627,216A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-09-627-216A-14

Query Match 1.0%; Score 10; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISSSP 835
Db 365 PRYSISSSP 374
|||||

RESULT 5

US-09-134-001C-4394
; Sequence 4394, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4394
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4394

Query Match 1.0%; Score 10; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAPFR 911
Db 489 GPGTGVAPFR 498
|||||

RESULT 6

US-07-642-002-2
; Sequence 2, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Bredt, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.

;; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
;; TITLE OF INVENTION: Oxide Synthase
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner, Birch, McKie & Beckett
;; STREET: One Thomas Circle, NW
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/642,002
;; FILING DATE: 19910118
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kagan, Sarah A.
;; REGISTRATION NUMBER: 32,141
;; REFERENCE/DOCKET NUMBER: 1107.033576
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 296-3500
;; TELEFAX: (202) 296-7830
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1429 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-642-002-2

Query Match 1.0%; Score 10; DB 1; Length 1429;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835
Db 1172 PRYSSSSP 1181

RESULT 7
US-08-365-486A-13
;; Sequence 13, Application US/08365486A
;; Patent No. 5834306
;; GENERAL INFORMATION:
;; APPLICANT: Webster, Keith A.
;; APPLICANT: Bishopric, Nanette H.
;; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
;; TITLE OF INVENTION: Therapeutic Constructs
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/365,486A
;; FILING DATE: 23-DEC-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 8255-0018

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1429 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-365-486A-13

Query Match 1.0%; Score 10; DB 2; Length 1429;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835
Db 1172 PRYSSSSP 1181

RESULT 8
US-08-319-866-11
;; Sequence 11, Application US/08319866
;; Patent No. 5929223
;; GENERAL INFORMATION:
;; APPLICANT: Tully, Timothy P.
;; APPLICANT: Yin, Jerry C.
;; APPLICANT: Regulski, Michael
;; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
;; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/319,866
;; FILING DATE: 7-OCT-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: CSHL94-03
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1429 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-319-866-11

Query Match 1.0%; Score 10; DB 2; Length 1429;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835
Db 1172 PRYSSSSP 1181

RESULT 9

US-08-880-342-13
; Sequence 13, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-13

Query Match 1.0%; Score 10; DB 4; Length 1429;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835
Db 1172 PRYISISSP 1181

RESULT 10

US-08-705-625-4
; Sequence 4, Application US/08705625
; Patent No. 5908756
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samie R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff

STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,625
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.57071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-705-625-4

Query Match 1.0%; Score 10; DB 2; Length 1430;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835
Db 1172 PRYISISSP 1181

RESULT 11

US-09-010-998-5
; Sequence 5, Application US/09010998
; Patent No. 6103872
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon
; APPLICANT: Jaffrey, Samie
; APPLICANT: Snowman, Adele
; APPLICANT: Eliasson, Mikael
; APPLICANT: Cohen, No. 6103872m
; TITLE OF INVENTION: CAPON, a protein that binds
; TITLE OF INVENTION: neuronal nitric oxide synthase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,998
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.73424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6103872e
US-09-010-998-5

Query Match 1.0%; Score 10; DB 3; Length 1430;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835
| | | | | | | | | |
DB 1172 PRYSSSSP 1181

RESULT 12
US-09-220-574-4
Sequence 4, Application US/09220574
Patent No. 6168926
GENERAL INFORMATION:
APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,574
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,625
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-220-574-4

Query Match 1.0%; Score 10; DB 4; Length 1430;
Best Local Similarity 100.0%; Pred. No. 0.79;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 826 PRYSSSSP 835
| | | | | | | | | |
DB 1172 PRYSSSSP 1181

RESULT 13
US-08-365-486A-21
Sequence 21, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1433 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-365-486A-21

Query Match 1.0%; Score 10; DB 2; Length 1433;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835
| | | | | | | | | |
DB 1176 PRYSSSSP 1185

RESULT 14
US-09-123-708-4
Sequence 4, Application US/09123708
Patent No. 6146887
GENERAL INFORMATION:
APPLICANT: SCHRAEDER, Juergen
APPLICANT: GOEDECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-4

Query Match 1.0%; Score 10; DB 4; Length 1433;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835
| | | | | | | | | |
Db 1176 PRYISISSP 1185

RESULT 15
US-09-123-624-4
; Sequence 4, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-123-624-4

Query Match 1.0%; Score 10; DB 4; Length 1433;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835
| | | | | | | | | |
Db 1176 PRYISISSP 1185

Search completed: May 29, 2003, 08:32:17
Job time : 30 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:30:56 ; Search time 54 Seconds
(without alignments)
1964.489 Million cell updates/sec

Title: US-10-031-146-2
Perfect score: 1048
Sequence: 1 TIKEMPQPTFGELKNLPL.....RLWLOLEEKGRYKDVWAG 1048

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 383519 seqs, 101223694 residues

Word size : 0

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	1.6	17	9	US-10-119-604C-20
2	13	1.2	597	9	Sequence 20, Appl
3	12	1.1	677	9	Sequence 2, Appli
4	10	1.0	588	10	Sequence 23, Appl
5	10	1.0	1433	9	Sequence 14, Appl
6	9	0.9	516	10	Sequence 4, Appl
7	9	0.9	679	9	Sequence 83, Appl
8	9	0.9	679	9	Sequence 84, Appl
9	9	0.9	679	9	Sequence 117, App
10	9	0.9	679	9	Sequence 118, App
11	9	0.9	679	9	Sequence 83, Appl
12	9	0.9	679	9	Sequence 84, Appl
13	9	0.9	679	9	Sequence 117, App
14	9	0.9	679	9	Sequence 118, App
15	9	0.9	679	9	Sequence 83, Appl
16	9	0.9	679	9	Sequence 84, Appl
17	9	0.9	679	9	Sequence 117, App
18	9	0.9	679	9	Sequence 118, App
19	9	0.9	679	9	Sequence 83, Appl

20	9	0.9	679	9	US-10-138-916-84	Sequence 84, Appl
21	9	0.9	679	9	US-10-138-916-117	Sequence 117, App
22	9	0.9	679	9	US-10-138-916-118	Sequence 118, App
23	9	0.9	679	9	US-09-976-800-83	Sequence 83, Appl
24	9	0.9	679	9	US-09-976-800-84	Sequence 84, Appl
25	9	0.9	679	9	US-09-976-800-117	Sequence 117, App
26	9	0.9	679	9	US-09-976-800-118	Sequence 118, App
27	9	0.9	679	10	US-09-911-781-11	Sequence 11, Appl
28	9	0.9	1144	9	US-09-870-759-124	Sequence 124, App
29	8	0.8	361	10	US-09-854-122-43	Sequence 43, Appl
30	8	0.8	362	10	US-09-854-122-42	Sequence 42, Appl
31	8	0.8	505	10	US-09-765-873A-12	Sequence 12, Appl
32	8	0.8	517	10	US-09-854-122-45	Sequence 45, Appl
33	8	0.8	519	10	US-09-854-122-44	Sequence 44, Appl
34	8	0.8	682	9	US-09-371-347-22	Sequence 22, Appl
35	8	0.8	689	9	US-09-371-347-48	Sequence 48, Appl
36	8	0.8	697	9	US-09-371-347-46	Sequence 46, Appl
37	8	0.8	698	9	US-09-371-347-2	Sequence 2, Appli
38	8	0.8	698	9	US-09-371-347-21	Sequence 21, Appl
39	8	0.8	698	9	US-09-371-347-42	Sequence 42, Appl
40	8	0.8	698	9	US-09-371-347-44	Sequence 44, Appl
41	7	0.7	7	9	US-10-145-415-43	Sequence 43, Appl
42	7	0.7	7	9	US-10-145-415-49	Sequence 49, Appl
43	7	0.7	23	10	US-09-864-761-47602	Sequence 47602, A
44	7	0.7	48	9	US-09-984-245-214	Sequence 214, App
45	7	0.7	48	9	US-09-966-262-214	Sequence 214, App

ALIGNMENTS

RESULT 1
US-10-119-604C-20
; Sequence 20, Application US/10119604C
; Publication No. US20030082772A1
; GENERAL INFORMATION:
; APPLICANT: Abell, Creed W.
; APPLICANT: Lewis, Duane A.
; TITLE OF INVENTION: Mutants of Monoamine Oxidase B
; FILE REFERENCE: D6048/D
; CURRENT APPLICATION NUMBER: US/119,604C
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/265,653
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of active site of wild type
; OTHER INFORMATION: P-450BM-3 enzyme
US-10-119-604C-20

QY	259	ITFLIAGHETTSGLLSF	275	Query Match	1.6%	Score 17;	DB 9;	Length 17;
Db	1	ITFLIAGHETTSGLLSF	17	Best Local Similarity	100.0%;	Pred. No. 5.8e-09;	Mismatches 0;	Indels 0;
				Matches 17;	Conservative 0;			Gaps 0;
RESULT 2								
US-09-778-319-2								
; Sequence 2, Application US/09778319								
; Patent No. US20020155560A1								
; GENERAL INFORMATION:								
; APPLICANT: POWELL, DAVID J.								
; APPLICANT: TEW, DAVID G.								
; TITLE OF INVENTION: A REDUCTASE								
; FILE REFERENCE: GH-70627-C1								
; CURRENT APPLICATION NUMBER: US/09/778,319								

; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 09/334,490
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 597
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-778-319-2

Query Match 1.2%; Score 13; DB 9; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPR 911
Db 454 INVPGTGVAPR 466

RESULT 3
US-09-371-347-23
; Sequence 23, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-347-23

Query Match 1.1%; Score 12; DB 9; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPR 910
Db 529 INVPGTGVAPR 540

RESULT 4
US-09-765-873A-14
; Sequence 14, Application US/09765873A
; Patent No. US20010053847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Helianthus tuberosus

US-09-765-873A-14

Query Match 1.0%; Score 10; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.77; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 826 PRYSISSSP 835
Db 365 PRYSISSSP 374

RESULT 5
US-10-224-249-14
; Sequence 14, Application US/10224249
; Publication No. US20030087867A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Ronald V.
; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis
; FILE REFERENCE: 2183-5233US
; CURRENT APPLICATION NUMBER: US/10/224,249
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: PCT/NL00/00482
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: EP 99202263.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/143,101
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(1433)
; OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-14

Query Match 1.0%; Score 10; DB 9; Length 1433;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISSSP 835
Db 1176 PRYSISSSP 1185

RESULT 6
US-09-740-046-4
; Sequence 4, Application US/09740046
; Patent No. US20020009751A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN MET
; FILE REFERENCE: EX00-044C
; CURRENT APPLICATION NUMBER: US/09/740,046
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/172,484
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/172,482
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/178,411
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/191,881
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: 60/192,142
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

LENGTH: 516
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-740-046-4

Query Match 0.9%; Score 9; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 FRPERFNP 382
Db 416 FRPERFNP 424

RESULT 7

US-10-138-838-83
Sequence 83, Application US/10138838
Publication No. US20030049821A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME

TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C

TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO

FILE REFERENCE: 1010-16

CURRENT APPLICATION NUMBER: US/10/138,838

CURRENT FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn version 3.1

SEQ ID NO 83

LENGTH: 679

TYPE: PRT

ORGANISM: CANDIDATROPICALIS

US-10-138-838-83

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834
Db 437 PRYSSISS 445

RESULT 8

US-10-138-838-84
Sequence 84, Application US/10138838
Publication No. US20030049821A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME

TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C

TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO

TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 679

TYPE: PRT

ORGANISM: CANDIDATROPICALIS

US-10-138-838-84

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834
Db 437 PRYSSISS 445

RESULT 9

US-10-138-838-117
Sequence 117, Application US/10138838
Publication No. US20030049821A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME

TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O

TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO

FILE REFERENCE: 1010-16

CURRENT APPLICATION NUMBER: US/10/138,838

CURRENT FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn version 3.1

SEQ ID NO 117

LENGTH: 679

TYPE: PRT

ORGANISM: CANDIDATROPICALIS

US-10-138-838-117

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834
Db 437 PRYSSISS 445

RESULT 10

US-10-138-838-118
Sequence 118, Application US/10138838
Publication No. US20030049821A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark

APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 679
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
US-10-138-838-118

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISS 834
|||||
DB 437 PRYSISS 445

RESULT 11
US-10-139-031-83
Sequence 83, Application US/10139031
Publication No. US20030049822A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Erich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 679
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
US-10-139-031-83

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISS 834
|||||
DB 437 PRYSISS 445

RESULT 12
US-10-139-031-84
Sequence 84, Application US/10139031
Publication No. US20030049822A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Erich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 84
LENGTH: 679
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
US-10-139-031-84

Query Match 0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISS 834
|||||
DB 437 PRYSISS 445

RESULT 13
US-10-139-031-117
Sequence 117, Application US/10139031
Publication No. US20030049822A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Erich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 117
LENGTH: 679
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
US-10-139-031-117

Query Match 0.9%; Score 9; DB 9; Length 679;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISS 834
 Db 437 PRYSSISS 445

RESULT 14

US-10-139-031-118
 ; Sequence 118, Application US/10139031
 ; Publication No. US2003004982A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, Ron C.
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Eshoo, Mark
 ; APPLICANT: Madduri, Krishna M.
 ; APPLICANT: Cornett, Cathy A.
 ; APPLICANT: Brenner, Alfred A.
 ; APPLICANT: Tang, Maria
 ; APPLICANT: Loper, John C.
 ; APPLICANT: Gleeson, Martin
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
 ; FILE REFERENCE: 1010-16
 ; CURRENT APPLICATION NUMBER: US/10/139,031
 ; CURRENT FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: US/09/976,800
 ; PRIOR FILING DATE: 2001-10-12
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 118
 ; LENGTH: 679
 ; TYPE: PRT
 ; ORGANISM: CANDIDATROPICALIS
 US-10-139-031-118

Query Match 0.9%; Score 9; DB 9; Length 679;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISS 834
 Db 437 PRYSSISS 445

RESULT 15

US-10-138-905-83
 ; Sequence 83, Application US/10138905
 ; Publication No. US20030068800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, Ron C.
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Eshoo, Mark
 ; APPLICANT: Madduri, Krishna M.
 ; APPLICANT: Cornett, Cathy A.
 ; APPLICANT: Brenner, Alfred A.
 ; APPLICANT: Tang, Maria
 ; APPLICANT: Loper, John C.
 ; APPLICANT: Gleeson, Martin
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
 ; FILE REFERENCE: 1010-16
 ; CURRENT APPLICATION NUMBER: US/10/138,905
 ; CURRENT FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: US/09/976,800

; PRIOR FILING DATE: 2001-10-12
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 83
 ; LENGTH: 679
 ; TYPE: PRT
 ; ORGANISM: CANDIDATROPICALIS
 US-10-138-905-83

Query Match 0.9%; Score 9; DB 9; Length 679;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISS 834
 Db 437 PRYSSISS 445

Search completed: May 29, 2003, 08:40:13
 Job time : 54 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:28:41 ; Search time 297 Seconds
(without alignments)
2275.018 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGLKNLPL.....RLWLQLEKGRYKDVNAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	24	US-10-031-146-2
2	1048	100.0	1048	24	US-10-031-241-35
3	1048	100.0	1048	24	US-10-031-695-2
4	1048	100.0	1049	1	PCT-US02-11954-2
5	1048	100.0	1049	21	US-09-791-537-53927
6	1048	100.0	1049	24	US-10-031-146-9

7	1048	100.0	1049	25	US-10-125-640-2
8	1048	100.0	1049	26	US-10-201-213-2
9	846	80.7	1049	22	US-09-856-339A-21
10	846	80.7	1049	24	US-10-018-730A-4
11	471	44.9	471	21	US-09-791-537-94076
12	463	44.2	464	1	PCT-US02-11954-3
13	463	44.2	464	25	US-10-125-640-3
14	458	43.7	458	21	US-09-791-537-116499
15	455	43.4	455	21	US-09-791-537-8264
16	370	35.3	471	21	US-09-791-537-71271
17	191	18.2	191	21	US-09-791-537-116501
18	28	2.7	222	12	US-08-882-163-9
19	28	2.7	222	12	US-08-882-163C-9
20	28	2.7	1054	1	PCT-US02-11954-4
21	28	2.7	1054	1	PCT-US02-11954-5
22	28	2.7	1054	21	US-09-791-537-139586
23	28	2.7	1054	25	US-10-125-640-5
24	28	2.7	1054	25	US-10-125-640-4
25	21	2.0	1061	1	PCT-US02-11954-6
26	21	2.0	1061	1	PCT-US02-11954-7
27	21	2.0	1061	21	US-09-791-537-139768
28	21	2.0	1061	25	US-10-125-640-6
29	21	2.0	1061	25	US-10-125-640-7
30	20	1.9	20	1	PCT-US98-07165-30
31	17	1.6	17	1	PCT-US99-05173-20
32	17	1.6	17	25	US-10-119-604C-20
33	16	1.5	659	21	US-09-791-537-71690
34	16	1.5	659	27	US-60-360-039-2318
35	16	1.5	661	21	US-09-791-537-20730
36	16	1.5	678	21	US-09-791-537-48331
37	16	1.5	678	27	US-60-360-039-2517
38	15	1.4	592	27	US-60-360-039-4874
39	15	1.4	592	27	US-60-360-039-7634
40	15	1.4	614	1	PCT-US02-13142-3234
41	15	1.4	614	25	US-10-128-714-3234
42	15	1.4	614	27	US-60-316-362-3234
43	15	1.4	626	18	US-09-417-507-41634
44	15	1.4	693	21	US-09-791-537-8203
45	15	1.4	693	24	US-10-021-425-38

ALIGNMENTS

RESULT 1

US-10-031-146-2
; Sequence 2, Application US/100311146
; GENERAL INFORMATION:
; APPLICANT: HAUER, Bernhard
; APPLICANT: PLEISS, Juergen
; APPLICANT: SCHWANEBERG, Ulrich
; APPLICANT: SCHMITT, Jutta
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the ox
; FILE REFERENCE: 50915
; CURRENT APPLICATION NUMBER: US/10/031,146
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect version 6.1
; SEQ ID NO 2
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-146-2

Query Match 100.0%; Score 1048; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TIKEMPQKTFGLKNLPLINTDKPQALMKIADELGEIFKFPAGRVTRYLSSORLIKE 60
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Db 1 TIKEMPQKTFGELKNLPLLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
QY 61 ACDESREFDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGHYHAMV 120
Db 61 ACDESREFDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGHYHAMV 120
QY 121 DIAVOLVKWERLNDADEHIEVPDMTRLTLDITGLCGFNYSYRQDPHFITSVMRA 180
Db 121 DIAVOLVKWERLNDADEHIEVPDMTRLTLDITGLCGFNYSYRQDPHFITSVMRA 180
QY 181 LDEAMNKLQRPNDPPAYDENKROQEDIKVNDLVDKIIADRKASGSDLLTHMLNG 240
Db 181 LDEAMNKLQRPNDPPAYDENKROQEDIKVNDLVDKIIADRKASGSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 300
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 300
QY 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
QY 361 HRDKTIWGDVDEEPRERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
Db 361 HRDKTIWGDVDEEPRERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
QY 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIGIPSPSTEQSAKKVRKKAENAHNT 480
Db 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIGIPSPSTEQSAKKVRKKAENAHNT 480
QY 481 PLLVLYGSMNGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540
Db 481 PLLVLYGSMNGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540
QY 541 PDNAKQFVDWLDQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600
Db 541 PDNAKQFVDWLDQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600
QY 601 GEADASDDPEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKLAKMHG 660
Db 601 GEADASDDPEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKLAKMHG 660
QY 661 AFSNTNVASKELQOQPGSARSTRHLEIPLPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 661 AFSNTNVASKELQOQPGSARSTRHLEIPLPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
QY 721 DASQOIRLEAEBEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 721 DASQOIRLEAEBEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYACEMKSFETIALLPSIRPRYYSISSSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTMLELLEKYACEMKSFETIALLPSIRPRYYSISSSPRVDEK 840
QY 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDPETPLIM 900
QY 901 VGPFGTVAPFRGTVQARKOLKEOGSLGEAHLYFCGRSPHEDYLYQEELENAQSGIITL 960
Db 901 VGPFGTVAPFRGTVQARKOLKEOGSLGEAHLYFCGRSPHEDYLYQEELENAQSGIITL 960
QY 961 HTAFSRMPNQPTYYQHVMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNQPTYYQHVMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
QY 1021 HOVSADARLWLOLEEKGRYAKDVWAG 1048
Db 1021 HOVSADARLWLOLEEKGRYAKDVWAG 1048

RESULT 2

US-10-031-241-35

; Sequence 35, Application US/10031241
; GENERAL INFORMATION:
; APPLICANT: Hauer, Bernhard
; APPLICANT: Schmid, Rolf D.
; APPLICANT: Schwaneberg, Ulrich
; TITLE OF INVENTION: Electron donor system for enzymes and its use in the biochemic
; FILE OF INVENTION: conversion of substrates
; FILE REFERENCE: M/40076
; CURRENT APPLICATION NUMBER: US/10/031,241
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07251
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; US-10-031-241-35

Query Match 100.0%; Score 1048; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 1 TIKEMPQKTFGELKNLPLLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
QY 61 ACDESREFDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGHYHAMV 120
Db 61 ACDESREFDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGHYHAMV 120
QY 121 DIAVOLVKWERLNDADEHIEVPDMTRLTLDITGLCGFNYSYRQDPHFITSVMRA 180
Db 121 DIAVOLVKWERLNDADEHIEVPDMTRLTLDITGLCGFNYSYRQDPHFITSVMRA 180
QY 181 LDEAMNKLQRPNDPPAYDENKROQEDIKVNDLVDKIIADRKASGSDLLTHMLNG 240
Db 181 LDEAMNKLQRPNDPPAYDENKROQEDIKVNDLVDKIIADRKASGSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 300
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 300
QY 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
QY 361 HRDKTIWGDVDEEPRERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
Db 361 HRDKTIWGDVDEEPRERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
QY 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIGIPSPSTEQSAKKVRKKAENAHNT 480
Db 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIGIPSPSTEQSAKKVRKKAENAHNT 480
QY 481 PLLVLYGSMNGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540
Db 481 PLLVLYGSMNGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540
QY 541 PDNAKQFVDWLDQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600
Db 541 PDNAKQFVDWLDQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600
QY 601 GEADASDDPEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKLAKMHG 660
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QY 661 AFSNTNVASKELQOQPGSARSTRHLEIPLPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 661 AFSNTNVASKELQOQPGSARSTRHLEIPLPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
QY 721 DASQOIRLEAEBEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

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Db 721 DASQIRLEAEKEKLAHLPLAKTVSVBELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Qy 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFESEFIALLPSPRIRYYSISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFESEFIALLPSPRIRYYSISSPRVDEK 840
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISPPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISPPQSEFTLPKDPETPLIM 900
Qy 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQEELENAQSEGIITL 960
Db 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQEELENAQSEGIITL 960
Qy 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Qy 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 3
US-10-031-695-2
; Sequence 2, Application US/10031695
; GENERAL INFORMATION:
; APPLICANT: Hauer, Bernhard
; APPLICANT: Pleiss, Jurgen
; APPLICANT: Schwaneberg, Ulrich
; APPLICANT: Schmitt, Jutta
; TITLE OF INVENTION: Modified cytochrome p450 monooxygenases
; FILE REFERENCE: M/40434
; CURRENT APPLICATION NUMBER: US/10/031, 695
; PRIOR FILING DATE: 2002-05-06
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-695-2

Query Match 100.0%; Score 1048; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOPKTFFGELKNPLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
Db 1 TIKEMPOPKTFFGELKNPLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
Qy 61 ACDESFPDKNLQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
Db 61 ACDESFPDKNLQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
Qy 121 DIAVOLVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYNFSFYRDQPHFITSMVRA 180
Db 121 DIAVOLVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYNFSFYRDQPHFITSMVRA 180
Qy 181 LDEAMNKLQANPDDPAYDENKQFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
Db 181 LDEAMNKLQANPDDPAYDENKQFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
Qy 241 KDPETGEPDDEINRYQIIFLIAGHETTSGLLSFALYFLVKNPHVQKAAEAARVLD 300
Db 241 KDPETGEPDDEINRYQIIFLIAGHETTSGLLSFALYFLVKNPHVQKAAEAARVLD 300
Qy 301 PVPYSQVKQKLYGVGVNLEALRWPTAPAFSLYAKEDTVLGGEYPLEKGEDELMLVLPOL 360
Db 301 PVPYSQVKQKLYGVGVNLEALRWPTAPAFSLYAKEDTVLGGEYPLEKGEDELMLVLPOL 360
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Qy 361 HRDRTIWGDDVEFRFRPERFENPSAIPQHAFFKPGNGORACIGQOQFALHEATVLGMLKH 420
Db 361 HRDRTIWGDDVEFRFRPERFENPSAIPQHAFFKPGNGORACIGQOQFALHEATVLGMLKH 420
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVVVAKSKKIPLGIPSPSTEQSAKKYKKAENAHT 480
Db 421 FDFEDHTNYELDIKETITLTKPEGFVVVAKSKKIPLGIPSPSTEQSAKKYKKAENAHT 480
Qy 481 PLVLVGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 481 PLVLVGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Qy 541 PDNAKQFVDMLDQASADEVKGVYVFGCGDKKNWATTYQKVPAFIDETLAAKGAENIADR 600
Db 541 PDNAKQFVDMLDQASADEVKGVYVFGCGDKKNWATTYQKVPAFIDETLAAKGAENIADR 600
Qy 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMHG 660
Db 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMHG 660
Qy 661 AFSTNVVASKELQOPGSARSTRHLELTELPEKASYQEGDHLGVIPRNYEGIVNRTARFGL 720
Db 661 AFSTNVVASKELQOPGSARSTRHLELTELPEKASYQEGDHLGVIPRNYEGIVNRTARFGL 720
Qy 721 DASQIRLEAEKEKLAHLPLAKTVSVBELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 721 DASQIRLEAEKEKLAHLPLAKTVSVBELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Qy 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFESEFIALLPSPRIRYYSISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFESEFIALLPSPRIRYYSISSPRVDEK 840
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISPPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISPPQSEFTLPKDPETPLIM 900
Qy 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQEELENAQSEGIITL 960
Db 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQEELENAQSEGIITL 960
Qy 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Qy 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
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RESULT 4

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PCT-US02-11954-2
; Sequence 2, Application PC/TUS0211954
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-W00
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)...(1049)
PCT-US02-11954-2

Query Match 100.0%; Score 1048; DB 1; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKFEAPGRVTRVYSSORLIKE 61
QY 61 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVOLVQKWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 180
DB 122 DIAVOLVQKWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEOSDILLTHMLNG 240
DB 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEOSDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 301
QY 301 PVPSTKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPO 360
DB 302 PVPSTKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPO 361
QY 361 HRDKTIWGDVVEEFPERFENPNSAIPQHAFKPFNGQACIGQAFALHEATLVGLMKLH 420
DB 362 HRDKTIWGDVVEEFPERFENPNSAIPQHAFKPFNGQACIGQAFALHEATLVGLMKLH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 481
QY 481 PLLVLYGNSWGTAEAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP 540
DB 482 PLLVLYGNSWGTAEAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP 541
QY 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDNKWTATYQKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDNKWTATYQKVPFIDETLAAKGAENIADR 601
QY 601 GEADASDDPEGTYEWRHMSDVAAYFNLDITENSEDNKSTLSLQFVDSAAWPLAKMHG 660
DB 602 GEADASDDPEGTYEWRHMSDVAAYFNLDITENSEDNKSTLSLQFVDSAAWPLAKMHG 661
QY 661 AFSTNVVASKELQOQCSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTRFGL 720
DB 662 AFSTNVVASKELQOQCSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTRFGL 721
QY 721 DASQOIRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPKHKVEL 780
DB 722 DASQOIRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPKHKVEL 781
QY 781 EALLKQAYKEQVLAARLTLMLELEKYPACEMKFSEFIALPSTIRPRYSISSSPRVDEK 840
DB 782 EALLKQAYKEQVLAARLTLMLELEKYPACEMKFSEFIALPSTIRPRYSISSSPRVDEK 841
QY 841 QASITVSVVSGAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
DB 842 QASITVSVVSGAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPFGTVAPFRGVQARKQKQSGSLGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 960
DB 902 VGPFGTVAPFRGVQARKQKQSGSLGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 961
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RESULT 5

US-09-791-537-53927

; Sequence 53927, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Dancer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09791,537

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53927

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: Bacillus megaterium

US-09-791-537-53927

Query Match 100.0%; Score 1048; DB 21; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKFEAPGRVTRVYSSORLIKE 61
QY 61 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVOLVQKWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 180
DB 122 DIAVOLVQKWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEOSDILLTHMLNG 240
DB 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEOSDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 301
QY 301 PVPSTKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPO 360
DB 302 PVPSTKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPO 361
QY 361 HRDKTIWGDVVEEFPERFENPNSAIPQHAFKPFNGQACIGQAFALHEATLVGLMKLH 420
DB 362 HRDKTIWGDVVEEFPERFENPNSAIPQHAFKPFNGQACIGQAFALHEATLVGLMKLH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 481
QY 481 PLLVLYGNSWGTAEAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP 540
DB 482 PLLVLYGNSWGTAEAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP 541
QY 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDNKWTATYQKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDNKWTATYQKVPFIDETLAAKGAENIADR 601
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QY 601 GEADSDDEGTYEWEHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADSDDEGTYEWEHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 661
QY 661 AFSTNVVASKELQOQPGSARSTRHLETELPEKASQYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQOQPGSARSTRHLETELPEKASQYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLERQAYKEQVLAKRLTLMLELKYACEMKFSEFIALLPSPRIRYISISSPRVDEK 840
Db 782 EALLERQAYKEQVLAKRLTLMLELKYACEMKFSEFIALLPSPRIRYISISSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEKGRYAKDVWAG 1049
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RESULT 6

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US-10-031-146-9
; Sequence 9, Application US/10031146
; GENERAL INFORMATION:
; APPLICANT: HAUER, Bernhard
; APPLICANT: PLEISS, Juergen
; APPLICANT: SCHWANEBERG, Ulrich
; APPLICANT: SCHMITT, Jutta
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the oxidat
; FILE OF INVENTION: organic substrates
; FILE REFERENCE: 50915
; CURRENT APPLICATION NUMBER: US/10/031,146
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect version 6.1
; SEQ ID NO 9
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-146-9
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Query Match 100.0%; Score 1048; DB 24; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
Db 2 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLQALFVRDFAGDGLFTSWTHKKNKKAHNILLPFSQOAMKGYHAMV 120
Db 62 ACDESFRDKNLQALFVRDFAGDGLFTSWTHKKNKKAHNILLPFSQOAMKGYHAMV 121
QY 121 DIAVOLQVQWERNLNADEHIEVPEDMTRLTDLTGLCGFNFRNSFYRDOHPHPIITSWRA 180
Db 122 DIAVOLQVQWERNLNADEHIEVPEDMTRLTDLTGLCGFNFRNSFYRDOHPHPIITSWRA 181
QY 181 LDEAMNKLQRANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 240
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Db 182 LDEAMNKLQRANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 241
QY 241 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
Db 242 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 301
QY 301 PVPYSYQVQKQKLVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGEDELWVLPOL 360
Db 302 PVPYSYQVQKQKLVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGEDELWVLPOL 361
QY 361 HRDKTIWGDVVEFRPERFENPSAIPQHAFAKPFNGQORACIGQOQFALHEATLVGLMMLKH 420
Db 362 HRDKTIWGDVVEFRPERFENPSAIPQHAFAKPFNGQORACIGQOQFALHEATLVGLMMLKH 421
QY 421 FOFEDHTNYELDIKETLTLKPEGFVVYKAKSKKPIPLGGIPSPSTEQSAKKVKKKAENAHNT 480
Db 422 FOFEDHTNYELDIKETLTLKPEGFVVYKAKSKKPIPLGGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLILVLYGSNNGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNHGP 540
Db 482 PLILVLYGSNNGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNHGP 541
QY 541 PONAQFVDWLQDQASADEVKGVYSVFGCGDKKNWATTYQKVPAFIDETTLAAGAENIADR 600
Db 542 PONAQFVDWLQDQASADEVKGVYSVFGCGDKKNWATTYQKVPAFIDETTLAAGAENIADR 601
QY 601 GEADSDDEGTYEWEHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADSDDEGTYEWEHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADPLAKMHG 661
QY 661 AFSTNVVASKELQOQPGSARSTRHLETELPEKASQYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQOQPGSARSTRHLETELPEKASQYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLERQAYKEQVLAKRLTLMLELKYACEMKFSEFIALLPSPRIRYISISSPRVDEK 840
Db 782 EALLERQAYKEQVLAKRLTLMLELKYACEMKFSEFIALLPSPRIRYISISSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEKGRYAKDVWAG 1049
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RESULT 7

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US-10-125-640-2
; Sequence 2, Application US/10125640
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/1K237-US3
; CURRENT APPLICATION NUMBER: US/10/125,640
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
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;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 60/340,602
;; PRIOR FILING DATE: 2001-12-12
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 1049
;; TYPE: PRT
;; ORGANISM: Bacillus megaterium
;; PUBLIC INFORMATION:
;; DATABASE ACCESSION NUMBER: GenBank / P14779
;; DATABASE ENTRY DATE: 1990-04-01
;; RELEVANT RESIDUES: (1)..(1049)
US-10-125-640-2

Query Match 100.0%; Score 1048; DB 25; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKEPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKEPGRVTRYLSSORLIKE 61

QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGYHAMV 120
Db 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGYHAMV 121

QY 121 DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNRYNSFYRDOPHPFITSMVRA 180
Db 122 DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNRYNSFYRDOPHPFITSMVRA 181

QY 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMNDLVDKIIADRKASGESQDOLLTHMLNG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMNDLVDKIIADRKASGESQDOLLTHMLNG 241

QY 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 300
Db 242 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 301

QY 301 PVPYSKQVKQLKYGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360
Db 302 PVPYSKQVKQLKYGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 361

QY 361 HRDKTIWGDVVEEFPRENFENSAIPQHAFFKPGNGORACIGQOQFALHEATLVGLMMLKH 420
Db 362 HRDKTIWGDVVEEFPRENFENSAIPQHAFFKPGNGORACIGQOQFALHEATLVGLMMLKH 421

QY 421 FDFEDHTNYELDIKETLTLKPGFVVKAKSKKIPILGGIPSPSTEQSAKKVKKKAENAHNT 480
Db 422 FDFEDHTNYELDIKETLTLKPGFVVKAKSKKIPILGGIPSPSTEQSAKKVKKKAENAHNT 481

QY 481 PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASVNGHP 540
Db 482 PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASVNGHP 541

QY 541 PDKAQFVDWLDOA SDADEVKGVRYSVFGCGDKNWTYYQKVPFADITETLAAGAENIADR 600
Db 542 PDKAQFVDWLDOA SDADEVKGVRYSVFGCGDKNWTYYQKVPFADITETLAAGAENIADR 601

QY 601 GEADASDDPEGTYEWEHMHWSDAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAKHG 660
Db 602 GEADASDDPEGTYEWEHMHWSDAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAKHG 661

QY 661 AFSTNVASKELOQPGSARSTRHEITELPKESAYOEGDHLGVIIPRYEGIVNRVTAARFGL 720
Db 662 AFSTNVASKELOQPGSARSTRHEITELPKESAYOEGDHLGVIIPRYEGIVNRVTAARFGL 721

QY 721 DASQQLRLAEAEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQLRLAEAEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781

QY 781 EALLEKQAKYEQVLAKRLTLMLELLEKYPACEMKSEFFALLPSIRPRYSSISSPRVDEK 840
Db 782 EALLEKQAKYEQVLAKRLTLMLELLEKYPACEMKSEFFALLPSIRPRYSSISSPRVDEK 841

RESULT 8

US-10-201-213-2
; Sequence 2, Application US/10201213
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; APPLICANT: Farinas, Edgardo
; APPLICANT: Glieder, Anton
; APPLICANT: Arnold, Frances
; APPLICANT: Schwanberg, Ulrich
; TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES
; FILE REFERENCE: 3369/IK238-US2
; CURRENT APPLICATION NUMBER: US/10/201,213
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 60/306,766
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/308,429
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(1049)
US-10-201-213-2

Query Match 100.0%; Score 1048; DB 26; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKEPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADELGEIFKEPGRVTRYLSSORLIKE 61

QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGYHAMV 120
Db 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQOAMKGYHAMV 121

QY 121 DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNRYNSFYRDOPHPFITSMVRA 180
Db 122 DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNRYNSFYRDOPHPFITSMVRA 181

QY 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMNDLVDKIIADRKASGESQDOLLTHMLNG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMNDLVDKIIADRKASGESQDOLLTHMLNG 241

QY 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 300
Db 242 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 301

QY 301 PVPYSKQVKQLKYGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360


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Db 302 PVPYSQVKQKLVGVNLEALRWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 361
QY 361 HRDKTWGDVEEFRRFENPNSAIPQHAEPKPGNGORACIGQOFALHEATLVLGWMLKH 420
Db 362 HRDKTWGDVEEFRRFENPNSAIPQHAEPKPGNGORACIGQOFALHEATLVLGWMLKH 421
QY 421 DFDHNTNYELDKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 480
Db 422 DFDHNTNYELDKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLYGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 541
QY 541 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 601
QY 601 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660
Db 602 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 661
QY 661 AFSTNVVASKELQOPGSASTRHLIELPKAESYQEGDHLGVIPRNYEGIVNVRTARFGL 720
Db 662 AFSTNVVASKELQOPGSASTRHLIELPKAESYQEGDHLGVIPRNYEGIVNVRTARFGL 721
QY 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGKYGTASNLYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGKYGTASNLYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPRGFVQARKQLKEQOQSLGEAHLFGCRSPHEDLYLQBELENAQSEGIITL 960
Db 902 VGPCTGVAPRGFVQARKQLKEQOQSLGEAHLFGCRSPHEDLYLQBELENAQSEGIITL 961
QY 1021 HOVSEADARLWLOOLEKGRYAKDVWAG 1048
Db 1022 HOVSEADARLWLOOLEKGRYAKDVWAG 1049
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RESULT 9

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US-09-856-339A-21
; Sequence 21, Application US/09856339A
; GENERAL INFORMATION:
; APPLICANT: Wong, Luet
; APPLICANT: Bell, Stephen
; APPLICANT: Carmichael, Angus
; TITLE OF INVENTION: PROCESS FOR OXIDISING TERPENES
; FILE REFERENCE: HO-P02196USO (10104571)
; CURRENT APPLICATION NUMBER: US/09/856,339A
; CURRENT FILING DATE: 2001-05-18
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/GB99/03873
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: GB 9825421.2
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
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; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1049)
; OTHER INFORMATION: Coding sequence
US-09-856-339A-21

Query Match 80.7%; Score 846; DB 22; Length 1049;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLLSSORLIKE 60
Db 2 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLLSSORLIKE 61
QY 61 ACDESREDKLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAKMKYHAMV 120
Db 62 ACDESREDKLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAKMKYHAMV 121
QY 121 DIAVOLVQKWERLNADSHIEVPEDMTRLTLDITGLCGFNRYFNRSFYRDQPHPTTSMVRA 180
Db 122 DIAVOLVQKWERLNADSHIEVPEDMTRLTLDITGLCGFNRYFNRSFYRDQPHPTTSMVRA 181
QY 181 LDEAMNKLQANPDPPAYDENKRFQFQEDIKVMNDLVDKIITADRKASGEQSDLLTHMLNG 240
Db 182 LDEAMNKLQANPDPPAYDENKRFQFQEDIKVMNDLVDKIITADRKASGEQSDLLTHMLNG 241
QY 241 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300
Db 242 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 301
QY 301 PVPYSQVKQKLVGVNLEALRWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 360
Db 302 PVPYSQVKQKLVGVNLEALRWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 361
QY 361 HRDKTWGDVEEFRRFENPNSAIPQHAEPKPGNGORACIGQOFALHEATLVLGWMLKH 420
Db 362 HRDKTWGDVEEFRRFENPNSAIPQHAEPKPGNGORACIGQOFALHEATLVLGWMLKH 421
QY 421 DFDHNTNYELDKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 480
Db 422 DFDHNTNYELDKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLYGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 541
QY 541 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 601
QY 601 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660
Db 602 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 661
QY 661 AFSTNVVASKELQOPGSASTRHLIELPKAESYQEGDHLGVIPRNYEGIVNVRTARFGL 720
Db 662 AFSTNVVASKELQOPGSASTRHLIELPKAESYQEGDHLGVIPRNYEGIVNVRTARFGL 721
QY 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGKYGTASNLYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGKYGTASNLYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPRGFVQARKQLKEQOQSLGEAHLFGCRSPHEDLYLQBELENAQSEGIITL 960
Db 902 VGPCTGVAPRGFVQARKQLKEQOQSLGEAHLFGCRSPHEDLYLQBELENAQSEGIITL 961
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QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADY 1020
|||||
Db 962 HTAFSEMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADY 1021
|||||
QY 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048
|||||
Db 1022 HOVSEADARLWLOLEEKGRYAKDVWAG 1049
|||||
RESULT 10
US-10-018-730A-4
; Sequence 4, Application US/10018730A
; GENERAL INFORMATION:
; APPLICANT: Luet, Wong
; APPLICANT: Jonathan, Jones
; TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
; FILE REFERENCE: P02353051 / 10112404 / N.762777B
; CURRENT APPLICATION NUMBER: US/10/018,730A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: GB 9914373.7
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/GB00/02379
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-018-730A-4

Query Match 80.7%; Score 846; DB 24; Length 1049;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
|||||
Db 2 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 61
|||||
QY 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 120
|||||
Db 62 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 121
|||||
QY 121 DIAVOLQKWERLNADEHIEVPEDMTRLTLDITGLCGFNRYNSFYRQDPHFITSMVRA 180
|||||
Db 122 DIAVOLQKWERLNADEHIEVPEDMTRLTLDITGLCGFNRYNSFYRQDPHFITSMVRA 181
|||||
QY 181 LDEAMNKLQANPPDPAIDENKROQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
|||||
Db 182 LDEAMNKLQANPPDPAIDENKROQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 241
|||||
QY 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEAAARVLD 300
|||||
Db 242 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEAAARVLD 301
|||||
QY 301 PVPYSYQVQKQKYGVGNLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360
|||||
Db 302 PAPSQYQVQKQKYGVGNLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 361
|||||
QY 361 HRDKTIWGDVDEEPRERENFENSAIPQAFKPFNGORACICQOQFALHEATLVLMMLKH 420
|||||
Db 362 HRDKTIWGDVDEEPRERENFENSAIPQAFKPFNGORACICQOQFALHEATLVLMMLKH 421
|||||
QY 421 FPFEDHTNYELDIKETLTLPKPGFVYVYKAKSKKIPILGGIPSPSTEOSAKKVRKKAENAHNT 480
|||||
Db 422 FPFEDHTNYELDIKETLTLPKPGFVYVYKAKSKKIPILGGIPSPSTEOSAKKVRKKAENAHNT 481
|||||
QY 481 PLLVLGYSNMGTAEGRDADLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
|||||
Db 482 PLLVLGYSNMGTAEGRDADLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
|||||
QY 541 PDNAKQFVDWLQASADEVKGVYRVFVCGCGDNWATTYQKVPFIDETLAAGAENIADR 600
|||||

Db 542 PDNAKQFVDWLQASADEVKGVYRVFVCGCGDNWATTYQKVPFIDETLAAGAENIADR 601
|||||
QY 601 GEADADSDDEGTYEWEHMHWSVAAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAMHG 660
|||||
Db 602 GEADADSDDEGTYEWEHMHWSVAAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAMHG 661
|||||
QY 661 AFSTNVVASKELQOPGSGARSSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTRARFGL 720
|||||
Db 662 AFSTNVVASKELQOPGSGARSSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTRARFGL 721
|||||
QY 721 DASQOIRLEAEKEKLAHLPLAKTVSVEELLOVVELQVDPVTRTQLRAMAAKTVCPPHKVEL 780
|||||
Db 722 DASQOIRLEAEKEKLAHLPLAKTVSVEELLOVVELQVDPVTRTQLRAMAAKTVCPPHKVEL 781
|||||
QY 781 EALLEKQAYKEOVLAKRLLTMELEKYPACEMKFEFFIALLSIRPRYYSISSPRVDEK 840
|||||
Db 782 EALLEKQAYKEOVLAKRLLTMELEKYPACEMKFEFFIALLSIRPRYYSISSPRVDEK 841
|||||
QY 841 QASITVSVVSGSAWGSYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
|||||
Db 842 QASITVSVVSGSAWGSYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901
|||||
QY 901 VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFGCRSPHEDYLYOELENAQSEGIITL 960
|||||
Db 902 VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFGCRSPHEDYLYOELENAQSEGIITL 961
|||||
QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADY 1020
|||||
Db 962 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADY 1021
|||||
QY 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048
|||||
Db 1022 HOVSEADARLWLOLEEKGRYAKDVWAG 1049
|||||

RESULT 11

US-09-791-537-94076

; Sequence 94076, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bloncomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Dancer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 94076

; LENGTH: 471

; TYPE: PRT

; ORGANISM: pdb 2HPDA

US-09-791-537-94076

Query Match 44.9%; Score 471; DB 21; Length 471;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
|||||
Db 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
|||||
QY 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 120
|||||
Db 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 120
|||||
QY 121 DIAVOLQKWERLNADEHIEVPEDMTRLTLDITGLCGFNRYNSFYRQDPHFITSMVRA 180
|||||
Db 121 DIAVOLQKWERLNADEHIEVPEDMTRLTLDITGLCGFNRYNSFYRQDPHFITSMVRA 180
|||||
QY 181 LDEAMNKLQANPPDPAIDENKROQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
|||||

Db 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLG 240
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 300
Db 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 300
Qy 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Qy 361 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
Db 361 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTQSAKKVR 471
Db 421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTQSAKKVR 471

RESULT 12
PCT-US02-11954-3
; Sequence 3, Application PC/TUS0211954
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-WO
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)...(464)
PCT-US02-11954-3

Query Match 44.2%; Score 463; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOKTFGELKKNPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSORLIKE 60
Db 2 TIKEMPOKTFGELKKNPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSORLIKE 61
Qy 61 ACDESREDFKNLSQALKFVRDPFAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 120
Db 62 ACDESREDFKNLSQALKFVRDPFAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 121
Qy 121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITIGLCGFNYRNFNSFYRDQPHFFITSMVRA 180
Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITIGLCGFNYRNFNSFYRDQPHFFITSMVRA 181
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLG 241
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 300
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 301
Qy 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360

Db 302 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 361
Qy 361 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
Db 362 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 421
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 463
Db 422 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 464

RESULT 13
US-10-125-640-3
; Sequence 3, Application US/10125640
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/1K237-US3
; CURRENT APPLICATION NUMBER: US/10/125,640
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)...(464)
US-10-125-640-3

Query Match 44.2%; Score 463; DB 25; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOKTFGELKKNPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSORLIKE 60
Db 2 TIKEMPOKTFGELKKNPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSORLIKE 61
Qy 61 ACDESREDFKNLSQALKFVRDPFAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 120
Db 62 ACDESREDFKNLSQALKFVRDPFAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 121
Qy 121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITIGLCGFNYRNFNSFYRDQPHFFITSMVRA 180
Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITIGLCGFNYRNFNSFYRDQPHFFITSMVRA 181
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLG 241
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 300
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVLD 301
Qy 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 302 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 361
Qy 361 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
Db 362 HRDRTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 421
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 463

Db 422 DFDHNTYELDIKETLTLPKPGFVVKAKSKKIPLGGIPSPST 454
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RESULT 14

US-09-791-537-116499
; Sequence 116499, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116499
; LENGTH: 458
; TYPE: PRT
; ORGANISM: pdb 1B5YA
US-09-791-537-116499

Query Match 43.7%; Score 458; DB 21; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE	60
Db	1	TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE	60
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
Db	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
QY	121	DIAVQLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSWRA	180
Db	121	DIAVQLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSWRA	180
QY	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG	240
Db	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG	240
QY	241	KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
Db	241	KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
QY	301	PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL	360
Db	301	PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL	360
QY	361	HRDKTIGWDVVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH	420
Db	361	HRDKTIGWDVVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH	420
QY	421	DFDHTNYELDIKETLTLPKPGFVVKAKSKKIPLGGI 458	
Db	421	DFDHTNYELDIKETLTLPKPGFVVKAKSKKIPLGGI 458	

RESULT 15

US-09-791-537-8264
; Sequence 8264, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8264
; LENGTH: 455
; TYPE: PRT
; ORGANISM: pdb 2B1HA
US-09-791-537-8264

Query Match 43.4%; Score 455; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE	60
Db	1	TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE	60
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
Db	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
QY	121	DIAVQLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSWRA	180
Db	121	DIAVQLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHFITSWRA	180
QY	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG	240
Db	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG	240
QY	241	KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
Db	241	KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
QY	301	PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL	360
Db	301	PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL	360
QY	361	HRDKTIGWDVVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH	420
Db	361	HRDKTIGWDVVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH	420
QY	421	DFDHTNYELDIKETLTLPKPGFVVKAKSKKIPL 455	
Db	421	DFDHTNYELDIKETLTLPKPGFVVKAKSKKIPL 455	

Search completed: May 29, 2003, 08:37:24
Job time : 301 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:29:06 ; Search time 105 Seconds
(without alignments)
2066.079 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGELKNPL.....RLWLQOLEKGRYAKDVWAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 995812 seqs, 207002235 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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7: /cgn2_6/ptodata/2/paa/US16_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1.6	1073	6	US-10-156-761-8117	Sequence 8117, Ap
2	1.5	659	6	US-10-369-493-2518	Sequence 2518, Ap
3	1.5	678	6	US-10-369-493-2517	Sequence 2517, Ap
4	1.4	592	6	US-10-369-493-4874	Sequence 4874, Ap
5	1.5	592	6	US-10-369-493-7634	Sequence 7634, Ap
6	1.4	1077	6	US-10-214-446-24	Sequence 24, Appl
7	1.1	504	6	US-10-156-761-14954	Sequence 14954, A
8	1.1	676	6	US-10-219-051B-12757	Sequence 12757, A
9	1.1	677	7	US-60-440-068-572	Sequence 572, App
10	1.1	682	6	US-10-148-907A-23	Sequence 23, Appl
11	1.1	691	6	US-10-369-493-22034	Sequence 22034, A
12	1.1	689	6	US-10-424-599-187294	Sequence 187294, A
13	1.0	691	6	US-10-424-599-191313	Sequence 191313, A
14	1.1	1352	6	US-10-156-761-9867	Sequence 9867, Ap
15	1.0	588	6	US-10-188-523B-14	Sequence 14, Appl
16	1.0	588	6	US-10-188-523C-14	Sequence 14, Appl
17	1.0	629	6	US-10-092-411A-4394	Sequence 4394, Ap
18	1.0	719	6	US-10-425-114-70174	Sequence 70174, A
19	1.0	1199	7	US-60-452-680-23982	Sequence 23982, A
20	1.0	1199	7	US-60-453-135-14960	Sequence 14960, A
21	1.0	1199	7	US-60-453-050-14960	Sequence 14960, A
22	1.0	1199	7	US-60-455-444-8116	Sequence 8116, Ap
23	1.0	1199	7	US-60-465-241-8116	Sequence 8116, Ap
24	1.0	1429	5	US-09-661-258-2	Sequence 2, Appl
25	1.0	1434	5	US-09-661-258-1	Sequence 1, Appl
26	0.9	199	5	US-09-675-784A-13060	Sequence 13060, A

27	9	0.9	383	6	US-10-425-114-47717	Sequence 47717, A
28	9	0.9	413	6	US-10-425-114-44757	Sequence 44757, A
29	9	0.9	510	1	PCT-US02-40225-3240	Sequence 3240, Ap
30	9	0.9	510	6	US-10-320-797-3240	Sequence 3240, Ap
31	9	0.9	538	6	US-10-425-114-52887	Sequence 52887, A
32	9	0.9	648	6	US-10-272-017A-2	Sequence 2, Appl
33	9	0.9	648	6	US-10-272-017A-3	Sequence 3, Appl
34	9	0.9	648	6	US-10-272-017A-5	Sequence 5, Appl
35	9	0.9	648	6	US-10-272-017A-6	Sequence 6, Appl
36	9	0.9	679	6	US-10-400-902-11	Sequence 11, Appl
37	9	0.9	679	6	US-10-405-660-83	Sequence 83, Appl
38	9	0.9	679	6	US-10-405-660-84	Sequence 84, Appl
39	9	0.9	679	6	US-10-405-660-117	Sequence 117, App
40	9	0.9	679	6	US-10-405-660-118	Sequence 118, App
41	9	0.9	717	6	US-10-369-493-4154	Sequence 4154, Ap
42	9	0.9	1144	5	US-09-751-708A-124	Sequence 124, App
43	9	0.9	1144	5	US-09-661-258-5	Sequence 5, Appl
44	8	0.8	82	6	US-10-424-599-177345	Sequence 177345, A
45	8	0.8	151	6	US-10-219-051B-14077	Sequence 14077, A

ALIGNMENTS

RESULT 1
US-10-156-761-8117
; Sequence 8117, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10156.761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8117
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8117

Query Match 1.6%; Score 17; DB 6; Length 1073;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	260	TFLIAGHETTSGLLSFA	276
Db	269	TFLIAGHETTSGLLSFA	285

RESULT 2
US-10-369-493-2518
; Sequence 2518, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369.493
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2518
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2518

Query Match 1.5%; Score 16; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 914
|||||
Db 515 INVPGGTGVAPRGGFV 530

RESULT 3

US-10-369-493-2517
; Sequence 2517, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2517
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2517

Query Match 1.5%; Score 16; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 914
|||||
Db 534 INVPGGTGVAPRGGFV 549

RESULT 4

US-10-369-493-4874
; Sequence 4874, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4874
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4874

Query Match 1.4%; Score 15; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 913
|||||
Db 449 INVPGGTGVAPRGGFV 463

RESULT 5

US-10-369-493-7634
; Sequence 7634, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7634
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7634

Query Match 1.4%; Score 15; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 913
|||||
Db 449 INVPGGTGVAPRGGFV 463

RESULT 6

US-10-214-446-24
; Sequence 24, Application US/10214446
; GENERAL INFORMATION:
; APPLICANT: Weiner, David
; APPLICANT: Burk, Mark J.
; APPLICANT: Hitchman, Tim
; APPLICANT: Pujol, Catherine
; APPLICANT: Richardson, Toby
; APPLICANT: Short, Jay M.
; TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 09010-500001
; CURRENT APPLICATION NUMBER: US/10/214,446
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/309,497
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-214-446-24

Query Match 1.4%; Score 15; DB 6; Length 1077;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 TFLIAGHETTSGLLS 274

Db 266 TFLIAGHETTSGLLS 280
|||||

RESULT 7
US-10-156-761-14954
; Sequence 14954, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14954
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14954

Query Match 1.1% Score 12; DB 6; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 404 QFALHEATVIG 415
|||||
Db 430 QFALHEATVIG 441

RESULT 8
US-10-219-051B-12757
; Sequence 12757, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 12757
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / BAB18572
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-12757

Query Match 1.1% Score 12; DB 6; Length 676;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPF 910
|||||
Db 528 INVPGGTGVAPF 539

RESULT 9
US-60-440-068-572
; Sequence 572, Application US/60440068
; GENERAL INFORMATION:
; APPLICANT: NADLER, STEVEN G.
; APPLICANT: CARMAN, JULIE
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
; FILE REFERENCE: 3053-4191
; CURRENT APPLICATION NUMBER: US/60/440,068
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 572
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-440-068-572

Query Match 1.1% Score 12; DB 7; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPF 910
|||||
Db 529 INVPGGTGVAPF 540

RESULT 10
US-10-148-907A-23
; Sequence 23, Application US/10148907A
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Compositions and Methods for Halogenation Reactions
; FILE REFERENCE: S-31082A
; CURRENT APPLICATION NUMBER: US/10/148,907A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/228801
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/219343
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-148-907A-23

Query Match 1.1% Score 12; DB 6; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPF 910
|||||
Db 533 INVPGGTGVAPF 544

RESULT 11
US-10-369-493-22034
; Sequence 22034, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22034
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22034

Query Match 1.1%; Score 12; DB 6; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAPRGF 913
DB 540 GPGTGVAPRGF 551
|||||

RESULT 12
US-10-424-599-187294
; Sequence 187294, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187294
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(689)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140138C.1.pap
US-10-424-599-187294

Query Match 1.0%; Score 11; DB 6; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 836
DB 466 PRYSSSPR 476
|||||

RESULT 13
US-10-424-599-191313
; Sequence 191313, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191313
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_14776C.1.pap
US-10-424-599-191313

Query Match 1.0%; Score 11; DB 6; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 836
DB 468 PRYSSSPR 478
|||||

RESULT 14
US-10-156-761-9867
; Sequence 9867, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIKAWA, JUN
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9867
; LENGTH: 1352
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9867

Query Match 1.0%; Score 11; DB 6; Length 1352;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 900 MVPGTGVAPF 910
DB 1210 MVPGTGVAPF 1220
|||||

RESULT 15
US-10-188-523B-14
; Sequence 14, Application US/10188523B
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US DIVCIP
; CURRENT APPLICATION NUMBER: US/10/188,523B
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-10-188-523B-14

Query Match 1.0%; Score 10; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 835

Db |||||
 365 PRYSSSP 374

Search completed: May 29, 2003, 08:39:13
Job time : 106 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:37:32 ; Search time 99 Seconds
(without alignments)
2181.186 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLQLEKGRYKDVWAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protein.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	2.7	29	Q9AE23	Q9ae23 bacillus me
2	17	1.6	730	Q8X1W0	Q8x1w0 coriolus ve
3	15	1.4	693	Q00141	Q00141 aspergillus
4	14	1.3	690	Q9HGL4	Q9hgl4 phanerocha
5	14	1.3	736	Q9HDP2	Q9hdp2 phanerocha
6	13	1.2	558	Q94613	Q94613 schizosacch
7	13	1.2	597	Q9UHB4	Q9uhb4 homo sapien
8	13	1.2	597	Q96BC6	Q96bc6 homo sapien
9	13	1.2	605	Q32214	Q32214 bacillus su
10	13	1.2	607	Q9KF76	Q9kf76 bacillus ha
11	13	1.2	629	Q9P4E1	Q9p4e1 cunningham
12	13	1.2	671	Q9HFD3	Q9hfd3 rhizopus st
13	13	1.2	710	Q9P4E2	Q9p4e2 cunningham
14	13	1.2	1066	Q9Y8G7	Q9y8g7 fusarium ox
15	12	1.1	527	Q9RD76	Q9rd76 streptomyce
16	12	1.1	696	Q8R0Y3	Q8r0y3 mus musculus

17	12	1.1	759	3	Q9C498	Q9c498 rhodotorula
18	11	1.0	506	10	Q96560	Q96560 helianthus
19	11	1.0	681	10	Q48937	Q48937 petroselinu
20	11	1.0	692	10	Q43235	Q43235 vicia sativ
21	11	1.0	692	10	Q9AU08	Q9au08 populus bal
22	11	1.0	692	10	Q9SB48	Q9sb48 arabidopsis
23	11	1.0	699	10	Q48938	Q48938 petroselinu
24	11	1.0	703	10	Q8VX49	Q8vx49 triticum ae
25	11	1.0	704	10	Q04434	Q04434 pisum sativ
26	11	1.0	712	10	Q9AU06	Q9au06 populus bal
27	11	1.0	719	10	Q40916	Q40916 pseudotsuga
28	11	1.0	1115	3	Q9HGE0	Q9hg0 gibberella
29	10	1.0	238	10	Q42830	Q42830 helianthus
30	10	1.0	541	5	Q961A7	Q961a7 drosophila
31	10	1.0	582	5	Q9V5J5	Q9vsj5 drosophila
32	10	1.0	585	5	Q9U2Y8	Q9u2y8 caenorhabdi
33	10	1.0	588	10	Q96561	Q96561 helianthus
34	10	1.0	612	16	Q9PD80	Q9pd80 xyella fas
35	10	1.0	614	16	Q9KUX4	Q9kux4 vibrio chol
36	10	1.0	683	10	Q24424	Q24424 papaver som
37	10	1.0	687	5	Q9NKV3	Q9nkV3 bombyx mori
38	10	1.0	712	10	Q9AU07	Q9au07 populus bal
39	9	0.9	120	2	Q85652	Q85652 micromonos
40	9	0.9	120	2	Q85654	Q85654 pseudonocar
41	9	0.9	317	10	Q9SB29	Q9sb29 oryza sativ
42	9	0.9	327	10	Q41736	Q41736 zea mays (m
43	9	0.9	506	10	Q9ATU8	Q9atu8 lolium rigi
44	9	0.9	513	10	Q9ATU7	Q9atu7 lolium rigi
45	9	0.9	701	5	P91655	P91655 drosophila

ALIGNMENTS

RESULT 1

Q9AE23 ID Q9AE23 PRELIMINARY; PRT; 29 AA.
AC Q9AE23;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Cytochrome P450BM-3 (Fragment).
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92184811; PubMed=1544926;
RA Shaw G.C., Fulco A.J.;
RT "Barbiturate-mediated regulation of expression of the cytochrome
RT P450BM-3 gene of Bacillus megaterium by Em3R1 protein.";
RL J. Biol. Chem. 267:5515-5526(1992).
DR EMBL; S87512; AAK19020.1; -.
FT NON_TER 29
SQ SEQUENCE 29 AA; 3283 MW; D97C2CFB57450EE8 CRC64;

Query Match 2.7%; Score 28; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 8.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLNTDKPVQA 28
|||||
DB 2 TIKEMPQKTFGELKNLPLNTDKPVQA 29

RESULT 2

Q8X1W0 ID Q8X1W0 PRELIMINARY; PRT; 730 AA.
AC Q8X1W0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Qy	899	IMVPGTGVAPRGRF	913	
Db	544	IMVPGTGVAPRGRF	558	
RESULT 4				
ID	Q9HG14	PRELIMINARY;	PRT;	690 AA.
AC	Q9HG14;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
DE	NADPH-dependent cytochrome P450 oxidoreductase	(EC 1.6.2.4)		
DE	(Fragment).			
DE	CPR.			
OS	Phanerochaete chrysosporium.			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Aphyllophorales; Corticiaceae; Phanerochaete.			
OX	NCBI_TaxID=5306;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BKMF-1767;			
RX	MEDLINE=20136378; PubMed=10672447;			
RA	yadav J.S., Loper J.C.;			
RT	"Cytochrome P450 oxidoreductase gene and its differentially terminated			
RT	cDNAs from the white rot fungus Phanerochaete chrysosporium.";			
RL	Curr. Genet. 37:65-73(2000).			
RL	EMBL; AF193062; RAG31351.1;			
DR	HSSP; P00388; IAMO.			
DR	InterPro; IPR003097; FAD_binding.			
DR	InterPro; IPR001094; Flavodoxin_like.			
DR	InterPro; IPR001226; Flavodoxin.			
DR	InterPro; IPR001709; FPN_cyt_redctse.			
DR	InterPro; IPR001433; Oxired_FAD/NAD(P).			
DR	Pfam; PF00567; FAD_binding; 1.			
DR	Pfam; PF00258; flavodoxin; 1.			
DR	Pfam; PF00175; NAD_binding; 1.			
DR	PRINTS; PR00369; FLAVODOXIN.			
DR	PRINTS; PR00371; FPNCR.			
KW	Oxidoreductase.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	690 AA; 76880 MW; 48B7D25BEC0F06B5 CRC64;		
Query Match 1.3%; Score 14; DB 3; Length 690;				
Best Local Similarity 100.08; Pred. No. 5.2e-05;				
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps				
Qy	902	GPGTGVAPRGRFVQ	915	
Db	528	GPGTGVAPRGRFVQ	541	
RESULT 5				
ID	Q9HDG2	PRELIMINARY;	PRT;	736 AA.
AC	Q9HDG2;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
DE	NADPH-dependent cytochrome P450 oxidoreductase	(EC 1.6.2.4).		
DE	(Fragment).			
DE	CPR.			
OS	Phanerochaete chrysosporium.			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Aphyllophorales; Corticiaceae; Phanerochaete.			
OX	NCBI_TaxID=5306;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BKMF-1767;			
RX	MEDLINE=20136378; PubMed=10672447;			
RA	yadav J.S., Loper J.C.;			
RT	"Cytochrome P450 oxidoreductase gene and its differentially terminated			
RT	cDNAs from the white rot fungus Phanerochaete chrysosporium.";			
RL	Curr. Genet. 37:65-73(2000).			

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DR EMBL; AF193061; AAC31350.1; -.
DR EMBL; AF193060; AAC31349.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redtctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase.
SQ
  Query Match      1.3%; Score 14; DB 3; Length 736;
  Best Local Similarity 100.0%; Pred. No. 5.5e-05;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 902 GPGTGVAPFRGFVQ 915
Db 574 GPGTGVAPFRGFVQ 587
  |||||
  [1]

RESULT 6
O94613 PRELIMINARY; PRT; 558 AA.
AC O94613;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative NADPH-cytochrome P450 reductase (EC 1.6.2.4).
GN SPAC1296.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Barrrell B.G., Rajandream M.A., Harris D., Seeger K.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME - NADP(+) + 2
CC FERROCYTOCHROME.
CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER
CC MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
DR EMBL; AL035439; CAB36512.2; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redtctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; FAD; NADP;
KW Endoplasmic reticulum; Membrane.
FT NP_BIND 524 542 NADP (RIBOSE PART) (BY SIMILARITY).
SQ SEQUENCE 558 AA; 64199 MW; 12D64991612E7E00 CRC64;

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Query Match      1.2%; Score 13; DB 3; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 897 PLIMVPGTGVAP 909
Db 414 PLIMVPGTGVAP 426
  |||||
  [1]

RESULT 7
Q9UHB4 PRELIMINARY; PRT; 597 AA.
AC Q9UHB4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADPH-dependent FMN and FAD containing oxidoreductase.
GN NRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092928; PubMed=10625700;
RA Paine M.J., Garner A.P., Powell D., Sibbald J., Sales M., Pratt N.,
RA Smith T., Tew D.G., Wolf C.R.;
RT "Cloning and Characterization of a Novel Human Dual Flavlin
RT Reductase.";
RL J. Biol. Chem. 275:1471-1478(2000).
DR EMBL; AF199509; AAF25205.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redtctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 597 AA; 66762 MW; 0D1340D7280A4D8F CRC64;

Query Match      1.2%; Score 13; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 IMVPGTGVAPFR 911
Db 454 IMVPGTGVAPFR 466
  |||||
  [1]

RESULT 8
Q96BC6 PRELIMINARY; PRT; 597 AA.
AC Q96BC6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADPH-dependent FMN and FAD containing oxidoreductase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015735; AAH15735.1; -.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001226; Flavodoxin.

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DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
SQ SEQUENCE 597 AA; 66776 MW; E1C340CF93A95534 CRC64;

Query Match 1.2%; Score 13; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPFR 911
Db 454 INVPGTGVAPFR 466

RESULT 9
O32214 PRELIMINARY; PRT; 605 AA.
AC O32214;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sulfite reductase [NADPH] flavoprotein alpha-component-like protein
DE (YVGR protein).
GN YVGR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessi  res P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser M., Goffeau A., Golligly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Weitzenecker T., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z99121; CAB15349.1; -.
DR HSSP: P00388; 1AMO.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.

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DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
KW Complete proteome.
SQ SEQUENCE 605 AA; 67259 MW; 486F512C0AED6217 CRC64;

Query Match 1.2%; Score 13; DB 16; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPFR 911
Db 462 INVPGTGVAPFR 474

RESULT 10
O9KF76 PRELIMINARY; PRT; 607 AA.
AC O9KF76;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sulfite reductase (NADPH).
GN BH0609.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125/JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001509; BAB04328.1; -.
DR HSSP: P00388; 1AMO.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctase.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Complete proteome.
SQ SEQUENCE 607 AA; 67865 MW; 3CD1B0EAA1DBFFBE CRC64;

Query Match 1.2%; Score 13; DB 16; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPFR 911
Db 464 INVPGTGVAPFR 476

RESULT 11
O9P4E1 PRELIMINARY; PRT; 629 AA.
AC O9P4E1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)

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DE (Fragment).
 OS Cunninghamella echinulata.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
 OC Cunninghamellaceae; Cunninghamella.
 OX NCBI_TaxID=76405;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-ATCC 26878;
 RX MEDLINE=20145435; PubMed=10679206;
 RA Yadav J.S., Loper J.C.;
 RT "Cloning and characterization of the cytochrome P450 oxidoreductase
 gene from the zygomycete fungus Cunninghamella.";
 RL Biochem. Biophys. Res. Commun. 268:345-353(2000).
 DR EMBL; AF195660; AAF89959.1; -;
 DR HSSP; P16435; 1B1C.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR Oxidoreductase.
 KW NON_TER 1
 FT 1
 SQ SEQUENCE 629 AA; 71388 MW; EC63589C857965A5 CRC64;
 Query Match 1.2%; Score 13; DB 3; Length 629;
 Best Local Similarity 100.0%; Pred. No. 0.00052;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 902 GPGTGVAPFRGFV 914
 Db 482 GPGTGVAPFRGFV 494
 |||||
 RESULT 12
 Q9HFV3 PRELIMINARY; PRT; 671 AA.
 AC Q9HFV3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE NADPH cytochrome P450 oxidoreductase isoenzyme 1 (EC 1.6.2.4).
 OS Rhizopus stolonifer (Rhizopus nigricans).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Rhizopus.
 OX NCBI_TaxID=4846;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP Kunik B., Tuan G., Breskvar K., Pompon D.;
 RT "Function cloning based on azole resistance in S. cerevisiae and
 characterization of R. nigricans redox carriers differentially
 involved in P450 dependent response to progesterone stress.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF290425; AAG23833.1; -;
 DR HSSP; P00388; 1AWO
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR PRINTS; PR00175; NAD_binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR Oxidoreductase.
 KW Oxidoreductase.
 SQ SEQUENCE 671 AA; 76205 MW; AAC1B236ACA5F88B CRC64;
 Query Match 1.2%; Score 13; DB 3; Length 671;
 QY 902 GPGTGVAPFRGFV 914
 Db 482 GPGTGVAPFRGFV 494
 |||||

Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 902 GPGTGVAPFRGFV 914
 Db 527 GPGTGVAPFRGFV 539
 |||||
 RESULT 13
 Q9P4E2 PRELIMINARY; PRT; 710 AA.
 AC Q9P4E2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).
 OS Cunninghamella elegans.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
 OC Cunninghamellaceae; Cunninghamella.
 OX NCBI_TaxID=4853;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-ATCC 36112;
 RX MEDLINE=20145435; PubMed=10679206;
 RA Yadav J.S., Loper J.C.;
 RT "Cloning and characterization of the cytochrome P450 oxidoreductase
 gene from the zygomycete fungus Cunninghamella.";
 RL Biochem. Biophys. Res. Commun. 268:345-353(2000).
 DR EMBL; AF195659; AAF89958.1; -;
 DR HSSP; P16435; 1B1C.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR Oxidoreductase.
 KW Oxidoreductase.
 SQ SEQUENCE 710 AA; 80021 MW; 8B3443AF5CDA3565 CRC64;
 Query Match 1.2%; Score 13; DB 3; Length 710;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 902 GPGTGVAPFRGFV 914
 Db 564 GPGTGVAPFRGFV 576
 |||||
 RESULT 14
 Q9Y8G7 PRELIMINARY; PRT; 1066 AA.
 AC Q9Y8G7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-
 hydroxylase) (P450foxy) [includes: cytochrome P450 505 (EC 1.14.14.1);
 NADPH-cytochrome P450 reductase (EC 1.6.2.4)].
 GN CYP505.
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=5507;
 RN [1]
 RC SEQUENCE FROM N.A.; PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RP STRAIN-MT-811.
 RX MEDLINE=20564350; PubMed=10995755;
 RA Kitazume T., Takaya N., Nakayama N., Shoun H.;
 RT "Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a

RT membrane-bound eukaryotic counterpart of Bacillus megaterium
 RT Cytochrome P450BM3.²
 RL J. Biol. Chem. 275:39734-39740(2000).
 RN [2]
 RP FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN-MT-811;
 RX MEDLINE=96271003; PubMed=8830036;
 RA Nakayama N., Takemae A., Shoun H.;
 RT "Cytochrome P450foxy, a catalytically self-sufficient fatty acid
 RT hydroxylase of the fungus Fusarium oxysporum."
 RL J. Biochem. 119:435-440(1996).
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST
 CC ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS.
 CC THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450.
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2
 CC FERROCYTOCHROME.
 CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
 CC P450 FAMILY.
 DR EMBL; AB030037; BAA82526.1; -.
 DR HSSP; P14779; 1BVY.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_redctase.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00175; NAD_binding; 1.
 DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 DR Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
 FT DOMAIN 1 480 CYTOCHROME P450
 FT DOMAIN 481 1066 NADPH-P-450 REDUCTASE.
 FT BINDING 407 407 HEME (BY SIMILARITY).
 SQ SEQUENCE 1066 AA; 117925 MW; 6B8123698C23DBA CRC64;
 Query Match 1.2%; Score 13; DB 3; Length 1066;
 Best Local Similarity 100.0%; Pred. No. 0.00085;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 259 ITFLIAGHETTS 271
 Db ITFLIAGHETTS 273
 RESULT 15
 Q9RD76 PRELIMINARY; PRT; 527 AA.
 AC Q9RD76;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative cytochrome P450.
 GN SC00801 OR SCE43.12.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Saunders D.C., Harris D.;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2);
 RC Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AL136502; CAB66201.1; -.
 DR HSSP; P14779; 1BVY.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR000217; Tubulin.
 DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR PROSITE; PS00227; TUBULIN; 1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;
 Query Match 1.1%; Score 12; DB 15; Length 527;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 404 QFALHEATLVLG 415
 Db 444 QFALHEATLVLG 455
 Search completed: May 29, 2003, 08:43:54
 Job time : 100 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:16.; Search time 74 Seconds
(without alignments)
1887.117 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	5457	100.0	1048	22 AAB31978	Amino acid sequenc
2	5457	100.0	1048	22 AAB46855	B. megaterium cyto
3	5457	100.0	1048	22 AAB46856	B. megaterium cyto
4	5457	100.0	1049	21 AAY93566	Amino acid sequenc
5	5457	100.0	1049	22 AAB31882	Amino acid sequenc
6	5450	99.9	1048	22 AAB31979	Amino acid sequenc
7	5449	99.9	1049	22 AAY72208	Bacillus megateriu
8	5444	99.8	1048	22 AAB31980	Amino acid sequenc
9	5440	99.7	1048	22 AAB31981	Amino acid sequenc
10	3154.5	57.8	1085	12 AAR11604	P450 17-alpha/P450

11	971.5	17.8	1144	9 AAB81334	Expression prod. o
12	968.5	17.7	1150	9 AAB81337	Expression prod. o
13	962.5	17.6	1150	9 AAB81335	Expression prod. o
14	916.5	16.8	1162	9 AAB81336	Expression prod. o
15	906.5	16.6	1132	9 AAB81338	Expression prod. o
16	778.5	14.3	678	23 ABB57261	Mouse ischaemic co
17	774.5	14.2	678	8 AAB70380	Plasmid pRF1 rat 1
18	772.5	14.2	678	8 AAB70578	NADPH cytochrome P
19	769	14.1	679	8 AAB70546	Sequence of rabbit
20	769	14.1	682	22 AAB82516	Rabbit NADH cytoch
21	766	14.0	680	22 AAU27786	Human full-length
22	766	14.0	685	22 AAU27958	Human contig polyp
23	761	13.9	677	22 AAB73901	Human derived cyto
24	761	13.9	677	22 AAB73902	Human derived cyto
25	747	13.7	676	20 AAY42286	Human P450 reducta
26	747	13.7	676	20 AAY27398	Human P450 reducta
27	747	13.7	676	23 AAO17538	Human P450(cytochr
28	746	13.7	671	14 AAR43583	Plant NADPH cytoch
29	737.5	13.5	616	20 AAY42287	Human anchoreless P
30	737.5	13.5	616	20 AAY27399	Human P450 reducta
31	726	13.3	623	9 AAB81339	Expression prod. o
32	725.5	13.3	679	22 ABB64462	Drosophila melanog
33	723.5	13.3	1169	16 AAR76544	Mitochondrial cyto
34	711.5	13.0	683	20 AAW85682	Poppy cytochrome P
35	711.5	13.0	883	20 AAW85680	Poppy cytochrome P
36	710.5	13.0	692	14 AAR43581	Plant NADPH cytoch
37	709	13.0	697	21 AAG35842	Arabidopsis thalia
38	709	13.0	701	21 AAG35841	Arabidopsis thalia
39	709	13.0	711	21 AAG35840	Arabidopsis thalia
40	705.5	12.9	588	23 AAE20656	Helianthus tuberos
41	705.5	12.9	588	23 AAE16392	Helianthus tuberos
42	703.5	12.9	704	20 AAW85683	Poppy cytochrome P
43	703.5	12.9	852	20 AAW85681	Poppy cytochrome P
44	695.5	12.7	712	14 AAR43582	Plant NADPH cytoch
45	678	12.4	1429	14 AAR44489	Sequence of all or

ALIGNMENTS

RESULT 1

AAB31978
ID AAB31978 standard; Protein; 1048 AA.

XX AAB31978;

AC AAB31978;

DT 15-MAY-2001 (first entry)

XX Amino acid sequence of a Bacillus P450 monooxygenase protein.

DE Cytochrome P450 monooxygenase; oxidation; indole; indigo; indirubin.

XX Bacillus megaterium.

XX WO200107630-A1.

PN 01-FEB-2001.

XX 27-JUL-2000; 2000WO-EP07253.

XX 27-JUL-1999; 99DE-10351115.

PR 18-NOV-1999; 99DE-1055605.

PR 22-MAR-2000; 2000DE-1014085.

XX (BADI) BASF AG.

XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

PI Li Q;

XX WPI; 2001-182800/18.

DR N-PSDB; AAF54832.

XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

PT

especially for converting indole to indigo, has wide substrate range -

Claim 3; Page 35-39; 54pp; German.

The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates:

CC optionally substituted mono- or poly-cyclic aromatic heterocyclics

CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or

CC optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many other substrates.

XX

SQ Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFEGELKPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60

DB 1 TIKEMPOKTFEGELKPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60

QY 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNIPLPSFSQAMKGYHAMV 120

DB 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNIPLPSFSQAMKGYHAMV 120

QY 121 DIAVOLVQWERLNADHEIEVPEDMTRLTDLTGLCGFNFRNSFYRDPHPPTSMVRA 180

DB 121 DIAVOLVQWERLNADHEIEVPEDMTRLTDLTGLCGFNFRNSFYRDPHPPTSMVRA 180

QY 181 LDEAMNKLQANPDDPAYDENKQFOEDIKVNDLVDKIADKASQSDLLTHMLNG 240

DB 181 LDEAMNKLQANPDDPAYDENKQFOEDIKVNDLVDKIADKASQSDLLTHMLNG 240

QY 241 KDPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVNKPHVLRKAAEAARVLD 300

DB 241 KDPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVNKPHVLRKAAEAARVLD 300

QY 301 PVPYSKQVQLKVGVLNEALRLNPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360

DB 301 PVPYSKQVQLKVGVLNEALRLNPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360

QY 361 HRDKTITGDDVEFERPERFENSAIPQAFKPGNGQRACIGQOAFALHEATLVLGMLKH 420

DB 361 HRDKTITGDDVEFERPERFENSAIPQAFKPGNGQRACIGQOAFALHEATLVLGMLKH 420

QY 421 FDPEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEQSAKKVRKKAENHT 480

DB 421 FDPEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEQSAKKVRKKAENHT 480

QY 481 PLLVLVGSNMGTAEGTARDIADAMSGFAPQVATLDHAGNLPRGAVLIVTASVNGHP 540

DB 481 PLLVLVGSNMGTAEGTARDIADAMSGFAPQVATLDHAGNLPRGAVLIVTASVNGHP 540

QY 541 PDNAKQFVDWLQASADEKVGVRYSVFGCGDKNWTYOKVPAFIDETLAAGAENIADR 600

DB 541 PDNAKQFVDWLQASADEKVGVRYSVFGCGDKNWTYOKVPAFIDETLAAGAENIADR 600

QY 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQPVDSAADMPKAMHG 660

DB 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQPVDSAADMPKAMHG 660

QY 661 AFSTNVVASKELQOPQASASTHLETELPEKASQYQEGDHLGVIPRNYGIVNRVARTFGL 720

DB 661 AFSTNVVASKELQOPQASASTHLETELPEKASQYQEGDHLGVIPRNYGIVNRVARTFGL 720

QY 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

DB 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALLPSIRPRYKSISSPRVDEK 840

DB 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALLPSIRPRYKSISSPRVDEK 840

QY 841 QASITVSVVSGRAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900

DB 841 QASITVSVVSGRAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900

QY 901 VPGTGVAPFRGVQARKQLKEGQSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 960

DB 901 VPGTGVAPFRGVQARKQLKEGQSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 960

QY 961 HTAFSRMPNQPTKYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020

DB 961 HTAFSRMPNQPTKYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020

QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048

DB 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 2

AAB46855

ID AAB46855 standard; Protein; 1048 AA.

XX AAB46855;

XX AC AC

XX 02-MAY-2001 (first entry)

XX B. megaterium cytochrome P450 monooxygenase BM-3 protein.

XX Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor; electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.

XX Bacillus megaterium.

XX WO200107573-A1.

XX 01-FEB-2001.

XX 27-JUL-2000; 2000WO-EP07251.

XX 27-JUL-1999; 99DE-1035115.

XX 10-MAR-2000; 2000DE-1011723.

XX (BADI) BASF AG.

XX Hauer B, Schmid RD, Schwaneberg U;

XX WPI; 2001-159709/16.

XX N-PSDB; AAF26268.

XX Novel electron donor system useful for the production of omega-hydroxylated fatty acids comprises an inorganic electron sink and a mediator which enables the electron transfer -

XX Claim 13b; Page 83-86; 94pp; German.

XX This invention describes a novel electron donor system (M1) that transfers electrons to an enzyme with redox properties comprising an inorganic, not electrode-bound, electron sink and a mediator which enable the electron transfer. The invention also describes (1) transferring (M2) oxygen to a hydrocarbon containing hydrogen donor molecule, where the hydrogen donor molecule is in a reaction medium comprising the oxygen transferring enzyme and (M1) in the presence of oxygen and incubating under suitable reaction conditions; (2) the enzymatic production (M3) of terminally or subterminally hydroxylated (position omega-1 to omega-4) fatty acids comprising: (i) mixing a hydroxylatable fatty acid or fatty acid derivative in the presence of (M1) and cytochrome P450 monooxygenase; and (ii) isolating the hydroxylated product; (3) a bioreactor useful for the production of omega-hydroxylated fatty acids as described in (2); and (4) detecting (M4) fatty acid-monooxygenases comprising: (1) contacting the analyte with a omega-hydroxylatable fatty

CC acid or a derivative comprising a terminal chromophore or fluorescent
CC label in (M); and (ii) qualitatively or quantitatively detecting the
CC signal. The invention is useful for the production of omega-hydroxylated
CC fatty acids and the detection of fatty acid monooxygenases. The
CC invention provides an alternative electron donor system of enzymes with
CC redox properties that is cheaper and more efficient, where the enzyme
CC comprises cytochrome 450.

XX
SQ Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNPLINTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSQRLIKE 60
DB 1 TIKEMPOKTFGELKNPLINTDKPVQALMKIADDELGEIFKFEAPGRVTRVYLSQRLIKE 60

QY 61 ACDESFPDKNLSQALKFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120
DB 61 ACDESFPDKNLSQALKFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120

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DB 121 DIAVOLVOKERLNADEHIEVPEDMTRLTDTIGLCGFNYRFSFYEDQPHPTITSMVRA 180

QY 181 LDEAMNKLRANPDPPAYDENKRFQEDIKVMNDLVDKIITADRKASGEQSDLLTHMLNG 240
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DB 241 KDPETGEPLDENIRYQIITFLIAGHETTSGLSFALYFLVKNPHVLQKAAEPAARVLD 300

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DB 301 PVPYSYQVKOLKYGVMVNEALRLWPTAPAFSLYAKEDTVLGCYPLEKGDMLVLPQL 360

QY 361 HRDKTIWDDVEEFREFENFENSAIPQHAFFKPGNGORACIGQOFALHEATLVLGWMLKH 420
DB 361 HRDKTIWDDVEEFREFENFENSAIPQHAFFKPGNGORACIGQOFALHEATLVLGWMLKH 420

QY 421 FDPEDHTNYELDIKEITLTKPEGVVKAASKKIPLGGIPSPSTEQSAKKYRKKAENAHNT 480
DB 421 FDPEDHTNYELDIKEITLTKPEGVVKAASKKIPLGGIPSPSTEQSAKKYRKKAENAHNT 480

QY 481 PLLVLVGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
DB 481 PLLVLVGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540

QY 541 PDNAKQFVWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAKGAENIADR 600
DB 541 PDNAKQFVWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAKGAENIADR 600

QY 601 GEADASDDFGTTEWEHNMWSDVAAFYFNLDIENSEDNKSTLSQFVDSAADPLAKMHG 660
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QY 661 AFTNIVVAKELQPGSARSSTRHLEIPLKPEASVQEGDHGVIPRNVGIVNRTAFGL 720
DB 661 AFTNIVVAKELQPGSARSSTRHLEIPLKPEASVQEGDHGVIPRNVGIVNRTAFGL 720

QY 721 DASQIRLEAEKEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780
DB 721 DASQIRLEAEKEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780

QY 781 EALLEKQAYEQVLAKRLTLMLELKYPCAMKFSFIALLPSTIRPRIYSISSPRVDEK 840
DB 781 EALLEKQAYEQVLAKRLTLMLELKYPCAMKFSFIALLPSTIRPRIYSISSPRVDEK 840

QY 841 QASITVSVSGEAWSGYGVKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
DB 841 QASITVSVSGEAWSGYGVKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900

QY 901 VGPCTGVAPPRGFQARKQLKEQQLSGEHLFGCRSPHEDYLYQEELNAOSEGIITL 960
DB 901 VGPCTGVAPPRGFQARKQLKEQQLSGEHLFGCRSPHEDYLYQEELNAOSEGIITL 960

QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
DB 961 HTAFSRMPNPKTYVQHVMEQDGKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020

QY 1021 HQVSEADARLWLOOLEBEKGRYAKDVWAG 1048
DB 1021 HQVSEADARLWLOOLEBEKGRYAKDVWAG 1048

RESULT 3
ID AAB46856
ID AAB46856 standard; Protein; 1048 AA.
XX AAB46856;
XX AC
XX DT 02-MAY-2001 (first entry)
XX DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.
XX KW Cytochrome P450 monooxygenase; BM-3; site-specific mutagenesis;
KW aliphatic carboxylic acid hydroxylation; fatty acid.
XX OS Bacillus megaterium.
XX PN W0200107574-A2.
XX PD 01-FEB-2001.
XX PF 27-JUL-2000; 2000WO-EP07252.
XX PR 27-JUL-1999; 99DE-1035115.
XX PR 10-MAR-2000; 2000DE-1011723.
XX PA (BADI) BASF AG.
XX PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI Li Q;
XX WPI; 2001-159710/16.
XX N-PSDB; AAF26324.
XX PT New modified cytochrome P450 mono-oxygenase, useful for producing
PT hydroxylated aliphatic carboxylic acids and derivatives, has altered
PT substrate specificity -
XX Claim 3; Page 41-45; 49pp; German.
XX This invention describes a novel modified cytochrome P450 (I) having, as
XX a result of site-specific mutagenesis of its substrate-binding domain,
XX an altered substrate profile, relative to the wild-type, when used for
XX terminal and/or subterminal enzymatic hydroxylation of aliphatic
XX carboxylic acids. The invention also describes (i) nucleic acid (ii)
XX encoding (i), and its complement; (2) expression cassette (EC) containing
XX (ii) and control elements; (3) a vector containing at least one EC; (4)
XX recombinant microorganisms transformed with at least one vector of (3);
XX and (5) enzymatic production of terminally and/or subterminally
XX hydroxylated aliphatic carboxylic acids (A) using the microorganisms of
XX (4), or isolated (i). (i), and recombinant cells that express them, are
XX used to produce hydroxylated aliphatic carboxylic acids or their
XX derivatives (esters and amides). (i) have altered substrate specificity,
XX especially for hydroxylation of 8-12C fatty acids at the omega-1, -2
XX regioselectivity.
XX Sequence 1048 AA;
XX Query Match 100.0%; Score 5457; DB 22; Length 1048;
XX Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE	60
DB	1	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE	60
QY	61	ACDESFRDKNLSQLKLVFRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV	120
DB	61	ACDESFRDKNLSQLKLVFRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV	120
QY	121	DIATVQLVQKWERLNDAHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRQPHFITSWRA	180
DB	121	DIATVQLVQKWERLNDAHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRQPHFITSWRA	180
QY	181	LDEAMNKLQANPDPAVDENKQFOEDIKVNNDLVDKIIADRKASGEGSDLLTHMLNG	240
DB	181	LDEAMNKLQANPDPAVDENKQFOEDIKVNNDLVDKIIADRKASGEGSDLLTHMLNG	240
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLVD	300
DB	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLVD	300
QY	301	PVPSTKQVQLKYGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGEDELMLVLPOL	360
DB	301	PVPSTKQVQLKYGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGEDELMLVLPOL	360
QY	361	HRDKTIWGDVVEEPRERFENPSAIPQHAFKPFNGORACIGQOFALHEATLVLGMLKH	420
DB	361	HRDKTIWGDVVEEPRERFENPSAIPQHAFKPFNGORACIGQOFALHEATLVLGMLKH	420
QY	421	DFEDHTNYELDIKETLTKPGFVYVAKSKKIPLGIPSPSTEQSAKKVKKKAENHNT	480
DB	421	DFEDHTNYELDIKETLTKPGFVYVAKSKKIPLGIPSPSTEQSAKKVKKKAENHNT	480
QY	481	PLLVLYGSMGTAEAGTARDLADIAMSKGFAPOVAITLDHAGNLPREGAVLIIVTASYNCHP	540
DB	481	PLLVLYGSMGTAEAGTARDLADIAMSKGFAPOVAITLDHAGNLPREGAVLIIVTASYNCHP	540
QY	541	PONAKQFVDLQASADEKGVYRYSVFGGDKNNAWTTQKVPAFIDETLAAGAENIADR	600
DB	541	PONAKQFVDLQASADEKGVYRYSVFGGDKNNAWTTQKVPAFIDETLAAGAENIADR	600
QY	601	GRADASDDPEGTYEWRHMSDVAAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660
DB	601	GRADASDDPEGTYEWRHMSDVAAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660
QY	661	AFSTNVASKELQOQCSARSTRHEITLPEKASYOEGDHLGVIIPRYNBYVNRVTARFGL	720
DB	661	AFSTNVASKELQOQCSARSTRHEITLPEKASYOEGDHLGVIIPRYNBYVNRVTARFGL	720
QY	721	DASQIIRLEAESEKLAHLPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL	780
DB	721	DASQIIRLEAESEKLAHLPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL	780
QY	781	EALLEKQAYKEOVLAKRLTMLELLEKYPACEMKFSEFIALPISIRPRYISISSPRVDEK	840
DB	781	EALLEKQAYKEOVLAKRLTMLELLEKYPACEMKFSEFIALPISIRPRYISISSPRVDEK	840
QY	841	QASITVSVVSGEAWSGEYKGIASNYLAELQEGDTITCFITPQSEFTLPKDPETPLIM	900
DB	841	QASITVSVVSGEAWSGEYKGIASNYLAELQEGDTITCFITPQSEFTLPKDPETPLIM	900
QY	901	VGPSTGVAPFRGFOARQKQKQSGSLGAHLYFCGRSPHEDYLYQEELENAQSGIITL	960
DB	901	VGPSTGVAPFRGFOARQKQKQSGSLGAHLYFCGRSPHEDYLYQEELENAQSGIITL	960
QY	961	HTAFSRMPNQPTYYQHVMEQDGKKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADY	1020
DB	961	HTAFSRMPNQPTYYQHVMEQDGKKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADY	1020
QY	1021	HOVSADARLWLQOLEEKGRYAKDVWAG	1048
DB	1021	HOVSADARLWLQOLEEKGRYAKDVWAG	1048

RESULT 4			
AA93566			
ID	AA93566 standard; Protein; 1049 AA.		
XX	AA93566;		
AC	25-SEP-2000 (first entry)		
DT	Amino acid sequence of the P450-BM3 sequence.		
XX	Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;		
DE	infection; P450-BM3.		
KW	Unidentified.		
XX			
OS			
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 303	/note= "Val encoded by GCT"	
FT	Misc-difference 471	/note= "Val encoded by GCA"	
FT			
XX	WO200031273-A2.		
PN	02-JUN-2000.		
XX			
PD	19-NOV-1999; 99WO-GB03873.		
XX			
PF	19-NOV-1998; 98GB-0025421.		
XX	(ISIS-) ISIS INNOVATION LTD.		
PA	Wong LL, Bell SG, Carmichael AB;		
XX	WPI; 2000-451679/39.		
DR	N-PSDB; AAA46648.		
DR			
XX	Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or derivatives for preventing or treating infection in human or animal body comprises mutant haem-containing enzyme which has substitution of amino acid in the active site		
PS	Disclosure; Page 51-53; 63pp; English.		
XX			
CC	The specification describes a process for oxidizing an acyclic or cyclic terpene, a cycloalkene, or a derivative. The process comprises oxidizing the compound with a mutant haem-containing enzyme which comprises a substitution of an amino acid in the active site by an amino acid with a less polar side-chain. The process is useful for oxidizing an acyclic or cyclic terpene, a cycloalkene, or their derivatives. The process is also useful for producing an oxidation product useful for preventing or treating infection in a human or animal body. The present sequence represents the amino acid sequence of the P450-BM3 sequence. The protein is used to construct enzymes for use in the process of the invention.		
XX			
SQ	Sequence 1049 AA;		
Query Match 100.0%; Score 5457; DB 21; Length 1049;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE	60
DB	2	TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE	61
QY	61	ACDESFRDKNLSQLKLVFRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV	120
DB	62	ACDESFRDKNLSQLKLVFRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV	121
QY	121	DIATVQLVQKWERLNDAHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRQPHFITSWRA	180

Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDPHPFITSMVRA 181
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVYNDLVKIIADRKASQSDLLTHMLNG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVYNDLVKIIADRKASQSDLLTHMLNG 241
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 301
Qy 301 PVPYSKOVKOLKYVGMVINEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLVLPOL 360
Db 302 PVPYSKOVKOLKYVGMVINEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLVLPOL 361
Qy 361 HRDKTIWGDDVEEPRPERFENPSAIPQHAFFPGNGQRACIQGFALHEATVLGMLKH 420
Db 362 HRDKTIWGDDVEEPRPERFENPSAIPQHAFFPGNGQRACIQGFALHEATVLGMLKH 421
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVKRKAENAHNT 480
Db 422 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVKRKAENAHNT 481
Qy 481 PLLVLYGSNMGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSNMGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 541
Qy 541 PDNAKQFVMDLQASADEVKGVRYSVFSGCGDKNATTYQKVPFIDETLAAKGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRYSVFSGCGDKNATTYQKVPFIDETLAAKGAENIADR 601
Qy 601 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADMPPLAKMHG 660
Db 602 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADMPPLAKMHG 661
Qy 661 AFSTNVVASKELQOPGARSARSTRHLEIELPREASTQEGDHLGVIPRNYEGIVNRYTARFGL 720
Db 662 AFSTNVVASKELQOPGARSARSTRHLEIELPREASTQEGDHLGVIPRNYEGIVNRYTARFGL 721
Qy 721 DASQOIRLEAEEELAKHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEEELAKHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
Qy 781 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPSPRPRYSISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPSPRPRYSISSSPRVDEK 841
Qy 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDPETPLIM 901
Qy 901 VGPOTGVAPFRGFVOARKQLKEQOSLGAEHLFYGCGRSPHEDYLYQBELENAQSEGITL 960
Db 902 VGPOTGVAPFRGFVOARKQLKEQOSLGAEHLFYGCGRSPHEDYLYQBELENAQSEGITL 961
Qy 961 HTAFSRPNOPKTYVQHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1020
Db 962 HTAFSRPNOPKTYVQHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1021
Qy 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEKGRYAKDVWAG 1049

RESULT 5
AAB31882
ID AAB31882 standard; Protein; 1049 AA.
XX
AC AAB31882;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a Bacillus P450 monooxygenase protein.
XX

Kw Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin.
Xx Bacillus megaterium.
Os WO200107630-A1.
Xx 01-FEB-2001.
Pd 27-JUL-2000; 2000WO-EP07253.
Pf 27-JUL-1999; 99DE-10351115.
Pr 18-NOV-1999; 99DE-1055605.
Pr 22-MAR-2000; 2000DE-1014085.
Xx (BADI) BASF AG.
Pi Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
Li Q;
Xx WPI; 2001-182800/18.
Dr Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
Pt especially for converting indole to indigo, has wide substrate range -
Xx Disclosure; Page 41-44; 54pp; German.
Xx The present sequence represents a cytochrome P450 monooxygenase. The
Cc specification describes a modified cytochrome P450 monooxygenase which
Cc can oxidize at least one of the following types of substrates:
Cc optionally substituted mono- or poly-cyclic aromatic heterocyclics
Cc containing nitrogen, sulphur or oxygen; optionally substituted mono- or
Cc poly-cyclic aromatics; linear or branched alkanes or alkenes; or
Cc optionally substituted cycloalkanes or cycloalkenes. The modified
Cc cytochrome P450 monooxygenase are specifically used to oxidize indole
Cc to indigo and indorubicin. However, they may be used to oxidise many
Cc other substrates.

SQ Sequence 1049 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOKPTGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRVYSSORLIKE 60
Db 2 TIKEMPOKPTGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRVYSSORLIKE 61
Qy 61 ACDESREDKNLSQALKFVRDPAGDGLFTSWTHEKNWKAHNTLLPSFSQQAAMGYHAMV 120
Db 62 ACDESREDKNLSQALKFVRDPAGDGLFTSWTHEKNWKAHNTLLPSFSQQAAMGYHAMV 121
Qy 121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDPHPFITSMVRA 180
Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDPHPFITSMVRA 181
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVYNDLVKIIADRKASQSDLLTHMLNG 240
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVYNDLVKIIADRKASQSDLLTHMLNG 241
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 301
Qy 301 PVPYSKOVKOLKYVGMVINEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLVLPOL 360
Db 302 PVPYSKOVKOLKYVGMVINEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLVLPOL 361
Qy 361 HRDKTIWGDDVEEPRPERFENPSAIPQHAFFPGNGQRACIQGFALHEATVLGMLKH 420
Db 362 HRDKTIWGDDVEEPRPERFENPSAIPQHAFFPGNGQRACIQGFALHEATVLGMLKH 421
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVKRKAENAHNT 480

Db 422 DFDHNTYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 481
QY 481 PLLVLYGSMGTAEAGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540
Db 482 PLLVLYGSMGTAEAGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 541
QY 541 PDNAKQFVDWLQASADEVKGVYRVYFGCGDKNNWATYQKVPFIDETLAAKGAENIADR 600
Db 542 PDNAKQFVDWLQASADEVKGVYRVYFGCGDKNNWATYQKVPFIDETLAAKGAENIADR 601
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660
Db 602 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 661
QY 661 AFSTNVVSKELQOPGASRSTRHLELELPKEASYQEGDHLGVIIPRYEGIVNRVARTFGL 720
Db 662 AFSTNVVSKELQOPGASRSTRHLELELPKEASYQEGDHLGVIIPRYEGIVNRVARTFGL 721
QY 721 DASQQLRLEAEERKLAHLPLAKTVSVEELIQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQLRLEAEERKLAHLPLAKTVSVEELIQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKFSEFIALLPISIRPRYYSISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKFSEFIALLPISIRPRYYSISSPRVDEK 841
QY 841 QASITVSVYGSAWGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVYGSAWGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPGTGVPFRGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VGPGTGVPFRGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELENAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIIELDQGAHFYICGDSQMAPAVEATLMKSYADY 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIIELDQGAHFYICGDSQMAPAVEATLMKSYADY 1021
QY 1021 HOVSEADARLWLQOLEKGRYAKDVWAG 1048
Db 1022 HOVSEADARLWLQOLEKGRYAKDVWAG 1049

RESULT 6

AAB31979

ID AAB31979 standard; Protein; 1048 AA.

XX AC AAB31979;

XX DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a modified P450 monooxygenase protein.

XX DX Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX KW Bacillus megaterium.

XX OS

XX FH Key

XX FT Location/Qualifiers

XX FT Misc-difference 87

XX FT /note= "wild type Phe changed to Val."

XX XX

XX PN WO200107630-A1.

XX PD 01-FEB-2001.

XX XX 27-JUL-2000; 2000WO-BP07253.

XX PF 27-JUL-1999; 99DE-1035115.

XX PR 18-NOV-1999; 99DE-1055605.

XX PR 22-MAR-2000; 2000DE-1014085.

XX XX

XX PA (BADI) BASF AG.

XX XX

PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI Li Q;
XX WPI; 2001-182800/18.
DR Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
XX especially for converting indole to indigo, has wide substrate range -
PT Claim 5; Page -; 54pp; German.
XX The present sequence represents a modified cytochrome P450 monooxygenase.
XX The specification describes a modified cytochrome P450 monooxygenase
CC which can oxidize at least one of the following types of substrates:
CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or
CC optionally substituted cycloalkanes or cycloalkenes. The modified
CC cytochrome P450 monooxygenase are specifically used to oxidize indole
CC to indigo and indorubicin. However, they may be used to oxidise many
CC other substrates.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

SQ Sequence 1048 AA;

Query Match 99.9%; Score 5450; DB 22; Length 1048;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTKEMPQPKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 1 TTKEMPQPKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60
QY 61 ACDESREFDKNLSQLKVFVDFAGDGLFTSWTHEKNWKAHNILLFSQQAQMGVHAMV 120
Db 61 ACDESREFDKNLSQLKVFVDFAGDGLFTSWTHEKNWKAHNILLFSQQAQMGVHAMV 120
QY 121 DIAVLQVKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNFNSFYRQDPHFITSMVRA 180
Db 121 DIAVLQVKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNFNSFYRQDPHFITSMVRA 180
QY 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240
Db 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSEALYFLVKNPNVLOKAAEAAVLVD 300
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSEALYFLVKNPNVLOKAAEAAVLVD 300
QY 301 PVPSYKQVKQLKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL 360
Db 301 PVPSYKQVKQLKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL 360
QY 361 HRDKTIWGDVDEEFPERFENPSPAIPQRAKFPFGNGQACICQQQALHATVILGNMLKH 420
Db 361 HRDKTIWGDVDEEFPERFENPSPAIPQRAKFPFGNGQACICQQQALHATVILGNMLKH 420
QY 421 FDFEDHTNYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 480
Db 421 FDFEDHTNYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 480
QY 481 PLLVLYGSMGTAEAGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540
Db 481 PLLVLYGSMGTAEAGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540
QY 541 PDNAKQFVDWLQASADEVKGVYRVYFGCGDKNNWATYQKVPFIDETLAAKGAENIADR 600
Db 541 PDNAKQFVDWLQASADEVKGVYRVYFGCGDKNNWATYQKVPFIDETLAAKGAENIADR 600
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660
Db 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660

QY 661 AFSTNVASKELQPGSARSTRHLELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
 DB 661 AFSTNVASKELQPGSARSTRHLELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
 QY 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
 DB 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
 QY 781 EALLEKQAYKEQVLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 840
 DB 781 EALLEKQAYKEQVLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 840
 QY 841 QASITVSVVSGEAWSGYGYKGIASNYLAELQEGDITFCISTPQSEFTLPKDPETPLIM 900
 DB 841 QASITVSVVSGEAWSGYGYKGIASNYLAELQEGDITFCISTPQSEFTLPKDPETPLIM 900
 QY 901 VPGTGVAFRGVQARKQLKEQGSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
 DB 901 VPGTGVAFRGVQARKQLKEQGSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
 QY 961 HTAFSRMPNQPTYYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATILMKSADY 1020
 DB 961 HTAFSRMPNQPTYYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATILMKSADY 1020
 QY 1021 HQVSEADARLWQLQLEEKGRYAKOVWAG 1048
 DB 1021 HQVSEADARLWQLQLEEKGRYAKOVWAG 1048

RESULT 7

AA72208
 ID AAY72208 standard; Protein; 1049 AA.
 XX AC AAY72208;
 XX DT 24-APR-2001 (first entry)
 XX DE Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
 KW Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation;
 KW halogenated aromatic compound; electron transfer; putidaredoxin;
 KW putidaredoxin reductase; detoxification.
 XX OS Bacillus megaterium.
 XX PN WO200078973-A1.
 XX PD 28-DEC-2000.
 XX PF 19-JUN-2000; 2000WO-GB02379.
 XX PR 18-JUN-1999; 99GB-0014373.
 XX PR N-PSDB; AAD02365.
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Wong LL, Jones JP;
 XX DR WPI; 2001-071397/08.
 XX DR N-PSDB; AAD02365.
 XX PT New process for detoxifying environments contaminated with halo
 PT aromatic compounds comprises treating the affected area with a
 PT monooxygenase enzyme -
 XX PS Disclosure; Page 32-39; 42pp; English.
 XX CC The present invention relates to a process for enzymatically oxidising
 CC the halogenated aromatic compounds such as 1,2-dichlorobenzene,
 CC 1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4,5,
 CC 5'-pentachlorobiphenyl. The process comprises treating the polluted
 CC environment with a monooxygenase enzyme. A monooxygenase enzyme, P450cam,
 CC and its physiological electron transfer partners, putidaredoxin and
 CC putidaredoxin reductase, are used to oxidise the halogenated aromatic

CC compounds. Also mutants of the monooxygenase enzyme with substitutions in
 CC the active site have enhanced oxidation activity. The process and the
 CC transgenic plant or animal which expresses the monooxygenase enzyme are
 CC used for detoxifying the environment polluted with the halo aromatic
 CC compounds. The present sequence is a Bacillus megaterium monooxygenase
 CC enzyme, P450BM-3, which is homologous to the monooxygenase
 CC enzyme, P450cam.
 XX

SQ Sequence 1049 AA;

Query Match 99.9%; Score 5449; DB 22; Length 1049;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPQPTFGELKNLPLNTDKPVQALMKIADLGEIKFKFAPGRVTRYLSSQRIKE 60
 DB 2 TIKEMPQPTFGELKNLPLNTDKPVQALMKIADLGEIKFKFAPGRVTRYLSSQRIKE 61
 QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120
 DB 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 121
 QY 121 DIAVLQVQWERLNADLHEIEVPEDMTRLDITGLGCFNRFNSFYRDQPHPTITSMVRA 180
 DB 122 DIAVLQVQWERLNADLHEIEVPEDMTRLDITGLGCFNRFNSFYRDQPHPTITSMVRA 181
 QY 181 LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
 DB 182 LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 241
 QY 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300
 DB 242 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 301
 QY 301 PVPYSYQVQLKTVGVNLNEALRLNPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
 DB 302 PAPSYSYQVQLKTVGVNLNEALRLNPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 361
 QY 361 HRDRTIWDGDDVEEFRPERFENPSAIPQHAFKPGNGORACIGQOFALHEATVLGMMKLH 420
 DB 362 HRDRTIWDGDDVEEFRPERFENPSAIPQHAFKPGNGORACIGQOFALHEATVLGMMKLH 421
 QY 421 FDFEDHTNYELDIKETLTLLKPEGVYVAKSKKTIPLGGIPSPSTEQSAKKYKKAENAHNT 480
 DB 422 FDFEDHTNYELDIKETLTLLKPEGVYVAKSKKTIPLGGIPSPSTEQSAKKYKKAENAHNT 481
 QY 481 PLLVLYSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
 DB 482 PLLVLYSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
 QY 541 PDNAKQFVDWLDOASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAKGAENIADR 600
 DB 542 PDNAKQFVDWLDOASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAKGAENIADR 601
 QY 601 GEADASDDFEGTYEWEHMHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660
 DB 602 GEADASDDFEGTYEWEHMHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661
 QY 661 AFSTNVVASKELQPGSARSTRHLELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
 DB 662 AFSTNVVASKELQPGSARSTRHLELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 721
 QY 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
 DB 722 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
 QY 781 EALLEKQAYKEQVLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 840
 DB 782 EALLEKQAYKEQVLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 841
 QY 841 QASITVSVVSGEAWSGYGYKGIASNYLAELQEGDITFCISTPQSEFTLPKDPETPLIM 900
 DB 842 QASITVSVVSGEAWSGYGYKGIASNYLAELQEGDITFCISTPQSEFTLPKDPETPLIM 901

QY 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960
DB 902 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 961
QY 961 HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
DB 962 HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048
DB 1022 HOVSEADARLWLQOLEEKGRYAKDVWAG 1049

RESULT 8

ID AAB31980 standard; Protein; 1048 AA.

XX AAB31980;

XX 15-MAY-2001 (first entry)

XX Amino acid sequence of a modified P450 monooxygenase protein.

XX Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX Bacillus megaterium.

XX Key Location/Qualifiers

FT Misc-difference 87

FT Misc-difference 188 /note= "wild type Phe changed to Val"

FT Misc-difference 188 /note= "wild type Leu changed to Gln"

XX WO200107630-A1.

XX 01-FEB-2001.

XX 27-JUL-2000; 2000WO-BP07253.

XX 27-JUL-1999; 99DE-1035115.

PR 18-NOV-1999; 99DE-1055605.

PR 22-MAR-2000; 2000DE-1014085.

XX (BADI) BASF AG.

XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

PI Li Q;

XX WPI; 2001-182800/18.

XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful especially for converting indole to indigo, has wide substrate range -

XX Claim 5; Page -: 54pp; German.

XX The present sequence represents a modified cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: CC optionally substituted mono- or poly-cyclic aromatic heterocyclics CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or CC optionally substituted cycloalkanes or cycloalkenes. The modified CC cytochrome P450 monooxygenase are specifically used to oxidize indole CC to indigo and indorubicin. However, they may be used to oxidize many CC other substrates.

CC note: this sequence does not appear in the specification; it was created CC using information provided.

XX Sequence 1048 AA;

Query Match 99.8%; Score 5444; DB 22; Length 1048;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPQKTEGELKNLPLNTDKVQALMTADELGEIFKEAPEGRTVRYLSSORLIKE 60
DB 1 TIKEMPQKTEGELKNLPLNTDKVQALMTADELGEIFKEAPEGRTVRYLSSORLIKE 60
QY 61 ACDESFRDNISQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQQAQMGYHAMV 120
DB 61 ACDESFRDNISQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQQAQMGYHAMV 120
QY 121 DIAVOLVKWERLNADHEIEVPEDMTRTLDTIGLCGFNYRNSFYRQPHFPTSMVRA 180
DB 121 DIAVOLVKWERLNADHEIEVPEDMTRTLDTIGLCGFNYRNSFYRQPHFPTSMVRA 180
QY 181 LDEAMNKLQANPPDDPAYDENKRFQEDIKVMNDLVDKTIADRKASGQSDLLTHMLNG 240
DB 181 LDEAMNKLQANPPDDPAYDENKRFQEDIKVMNDLVDKTIADRKASGQSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300
DB 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300
QY 301 PVPYSKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL 360
DB 301 PVPYSKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL 360
QY 361 HRDKTIWGDVVEEFPERFENPSAIPQHAFKPFNGQKACIGQQFALHEATLVGLMMLKH 420
DB 361 HRDKTIWGDVVEEFPERFENPSAIPQHAFKPFNGQKACIGQQFALHEATLVGLMMLKH 420
QY 421 FDFEDHTNYELDIKETLTLPKGEFVVKAKSKIPGGIPSPSTESAKVKRKAENAHNT 480
DB 421 FDFEDHTNYELDIKETLTLPKGEFVVKAKSKIPGGIPSPSTESAKVKRKAENAHNT 480
QY 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPRREGAVLIVTASYNHP 540
DB 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPRREGAVLIVTASYNHP 540
QY 541 PDNAKQFVDWLDQASADEVKGVYRVFGCGDKNWTYQKVPAFIDETLAAGAENIADR 600
DB 541 PDNAKQFVDWLDQASADEVKGVYRVFGCGDKNWTYQKVPAFIDETLAAGAENIADR 600
QY 601 GEADASDDFEGTYEWRHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKHNG 660
DB 601 GEADASDDFEGTYEWRHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKHNG 660
QY 661 AFSTNVASKELQOPGSGARSSTRHLIELPKEASYOEGDHLGVIIPRYEGIVNRVTARFGL 720
DB 661 AFSTNVASKELQOPGSGARSSTRHLIELPKEASYOEGDHLGVIIPRYEGIVNRVTARFGL 720
QY 721 DASQQIRLEAEBEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTCPPKVEL 780
DB 721 DASQQIRLEAEBEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTCPPKVEL 780
QY 781 EALLEKQAYKEQVLAKRLTLMLELLKYPACEMKFEFTALLPSIRPRYSISSPRVDEK 840
DB 781 EALLEKQAYKEQVLAKRLTLMLELLKYPACEMKFEFTALLPSIRPRYSISSPRVDEK 840
QY 841 QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPPTPLIM 900
DB 841 QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPPTPLIM 900
QY 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960
DB 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960
QY 961 HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
DB 961 HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
QY 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048
DB 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048

RESULT 9

AAB31981
ID AAB31981 standard; Protein; 1048 AA.

XX AC AAB31981;

XX 15-MAY-2001 (first entry)

XX Amino acid sequence of a modified P450 monooxygenase protein.

XX Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX Bacillus megaterium.

XX Key Location/Qualifiers

FT Misc-difference 74

FT /note= "wild type Ala changed to Gly"

FT Misc-difference 87

FT /note= "wild type Phe changed to Val"

FT Misc-difference 188

FT /note= "wild type Leu changed to Gln"

XX WO200107630-A1.

XX 01-FEB-2001.

XX 27-JUL-2000; 2000WO-EP07253.

XX 27-JUL-1999; 99DE-1035115.

XX 18-NOV-1999; 99DE-1055605.

XX 22-MAR-2000; 2000DE-1014085.

XX (BADI) BASF AG.

XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

XX Li Q;

XX WPI; 2001-182800/18.

XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful especially for converting indole to indigo, has wide substrate range -

XX Claim 5; Page -: 54pp; German.

XX The present sequence represents a modified cytochrome P450 monooxygenase.

XX The specification describes a modified cytochrome P450 monooxygenase

XX which can oxidize at least one of the following types of substrates:

XX optionally substituted mono- or poly-cyclic aromatic heterocyclics

XX containing nitrogen, sulphur or oxygen; optionally substituted mono- or

XX poly-cyclic aromatics; linear or branched alkanes or alkenes; or

XX optionally substituted cycloalkanes or cycloalkenes. The modified

XX cytochrome P450 monooxygenase are specifically used to oxidize indole

XX to indigo and indorubicin. However, they may be used to oxidise many

XX other substrates.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 1048 AA;

Query Match 99.7%; Score 5440; DB 22; Length 1048;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1045; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGEKLNPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60

DB 1 TIKEMPQKTFGEKLNPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60

QY 61 ACDESREKLNQALKEFVRDAGDGLFTSTWTEKNKKKAHNILLPSFSQAMKGYHAMV 120

DB 61 ACDESREKLNQALKEFVRDAGDGLFTSTWTEKNKKKAHNILLPSFSQAMKGYHAMV 120

QY 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNSFYRDQPHPTTSMVRA 180
DB 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNSFYRDQPHPTTSMVRA 180
QY 181 LDEAMNKLORANPDDPAYDENKQFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
DB 181 LDEAMNKLORANPDDPAYDENKQFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLVD 300
DB 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLVD 300
QY 301 PVPSYQVQKLVKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGIEYPLEKGDMLVLPOL 360
DB 301 PVPSYQVQKLVKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGIEYPLEKGDMLVLPOL 360
QY 361 HRDKTIWGDVDEEPRPERFENPSAIPQHAFFKPGNGORACIGQGFALHEATLVGLMMLKH 420
DB 361 HRDKTIWGDVDEEPRPERFENPSAIPQHAFFKPGNGORACIGQGFALHEATLVGLMMLKH 420
QY 421 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGIPSPSTEQSAKKVKKKAENAHNT 480
DB 421 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGIPSPSTEQSAKKVKKKAENAHNT 480
QY 481 PLLVLYGSNMGTAEGTAROLDIAMSFGAPQVATLDSHAGNLPRREGAVLIVTASYNGHP 540
DB 481 PLLVLYGSNMGTAEGTAROLDIAMSFGAPQVATLDSHAGNLPRREGAVLIVTASYNGHP 540
QY 541 PDNAKQFVMDLQASADEVKGVYRVGCGDKNWTYQKPAFIDTFLAAGAENADR 600
DB 541 PDNAKQFVMDLQASADEVKGVYRVGCGDKNWTYQKPAFIDTFLAAGAENADR 600
QY 601 GEADASDDFEGTYEWRHMSDVAAFYFNLDIENSEDNKSTLSLQFVDSADMPKAKWHG 660
DB 601 GEADASDDFEGTYEWRHMSDVAAFYFNLDIENSEDNKSTLSLQFVDSADMPKAKWHG 660
QY 661 AFSTNVVASKELQPGSARSTRHLEIPELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
DB 661 AFSTNVVASKELQPGSARSTRHLEIPELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
QY 721 DASQQIRLEAEERKLAHLPLAKTVSVLELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
DB 721 DASQQIRLEAEERKLAHLPLAKTVSVLELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALLPISIRPRYYSISSPRVDEK 840
DB 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALLPISIRPRYYSISSPRVDEK 840
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
DB 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900
QY 901 VGPCTGVAPPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQELENAQSEGITL 960
DB 901 VGPCTGVAPPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQELENAQSEGITL 960
QY 961 HTAFSRMPNPKYVVOHVMEODGKLLIELDQGAHFYICGDSQMAPAVATLMKSYADV 1020
DB 961 HTAFSRMPNPKYVVOHVMEODGKLLIELDQGAHFYICGDSQMAPAVATLMKSYADV 1020
QY 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
DB 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 10
AAR11604

ID AAR11604 standard; Protein; 1085 AA.

XX AAR11604;

XX 20-JUN-1991 (first entry)

XX

[illegible]

Db 336 YLVNTPRIQKIQEELDTVIGRDRPRLSDRPQLPYLEAFLETFRHSSFPV-FTIPHST 394
QY 336 KEDTVLGGVEPLEKDELAVLIPOLHRDXTICGDVEEPRPERFENPS-AIQHAFKP-- 392
Db 395 IRDTSUNGFY-IPKGHCVFVQVQVNDHDELWGP-NEFRPERFLTSSGTLDKHLSEKVI 452
QY 393 -FGNGRACIGQOFALHEATLVLMMLKHDFEDHTNYELDIKET--LTLKP---EGFVV 446
Db 453 LFGLRKRCIGETIGRLEVFLEFLAILLQOOMEENVSPGKVDMTTPAYGLTLKHARCEHFQV 512
QY 447 KAKSK-----KIPLGIPSPSTEQS-AKVRKAENAHNTPLLVLYGSNMGTAEGTA 497
Db 513 QMRSSGPRASAAARMIQTAPPVKESSEFVKMKKTGRN-----IIVFYGSQTGAEEFA 567
QY 498 RDLADIAMSKGFAPOVATLDH-----AGNLPR--EGAVLIVTASY-NGHPPDNKQFVDM 550
Db 568 NLSKDAHRYGMRGMSADPEEDLADLSLPEIDKSLVFCMATYEGEDPTNAQDFYDM 627
QY 551 LQOASADEVKGVYSVFGCGDKNWTYQKVP-----FIDETLAAGAENIADRGADAD 607
Db 628 LQETDVD-LTGKFAVFLGNK-----TYEHENAMKGYVDORLEQLGAQRIEFLGLGDDG 682
QY 608 DREGTYEWEHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMH----- 659
Db 683 NLEEDFITWREQFPAVCEFFGVEATGEESIRQVELVYHE---DMDVAKVYTGEMGRK 739
QY 660 -----GAFSTNVASKELQOPGASRSTRHLEIEL-PKEASYOEGDHLGVIPIRN 706
Db 740 SYENQKPPFDKPNFLAAVTANRKLQ-GTERHLMHLELSDSKIRYESGDHVAVYIPAN 798
QY 707 YEGIVNRVTFRG--LDASQQIRLEAEKLAHLPLAKTVSVEELLYQVELQDPVTRTOL 764
Db 799 DSALVNOIGEILLGADLDVMSLNLDEESNKKHPPCPTTYRTALTYYLDTNP-PRTNV 857
QY 765 RAMAAKTVCPP-----HKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMFSEPI 818
Db 858 LYELAQYASEPSEQEDLHKWASSGEGKELYLSWVEARRHILAILQDYSRPPIDHLC 917
QY 819 ALLPSIRPRYSSTSSPRYDERQASITVSVWSGEAWSGEYKGIASNYL-AELQGD- 876
Db 918 ELLPLRQARYSIASSKVPNSVHCICAVAYEAKSGRVN-KGATSWLRKAKEPAGENG 976
QY 877 ----ITCFISTQSEFTLPKDPETPLIMVGPOTGVAPFRGVOARKQLKEOGOSLGEAHL 932
Db 977 GRALVPMFVR--KSOFRLPFKSTTVIMVGPOTGIAPFMGFIQERAWLREQKEVGETLL 1034
QY 933 YGCRSPHEDYLYOBELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKLIELLD 991
Db 1035 YGCRSRSEDIYLYREELARFHKDGLTQLNVAFSR-EQAHKYVYQHLKRDREHLMKLIH 1093
QY 992 Q-GAHFYICGDSQMAPAVEATLMKSYADHVOVSEADARLWLOOLEEKGRYAKDYWA 1047
Db 1094 EGAHYIVCGDARNMAKVONTFYDIVAEFGPMHTQAVDYVKMLTKGRYSLDWS 1150

RESULT 13

AAP81335

ID AAP81335 standard; protein; 1150 AA.

XX

AC AAP81335;

XX

DT 19-OCT-1990 (first entry)

XX

DE Expression prod. of plasmid pALP1.

XX

KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;

KW industrial waste.

XX

PN JP63044888-A;

XX

PD 25-FEB-1988.

XX

PF 12-AUG-1986; 86JP-0187713.
PR 12-AUG-1986; 86JP-0187713.
XX (AGEN) AGENCY OF IND SCI TECH.
XX WPI; 1988-094816/14.
DR N-PSDB; AAN81744.
XX
PT Chinaera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
PT and NADPH-cytochrome p-450 reduction enzyme
XX Disclosure; ; p; Japanese.
CC See also AAN81743 and AAN81745-48.
XX
SQ Sequence 1150 AA;

Query Match 17.6%; Score 962.5; DB 9; Length 1150;
Best Local Similarity 28.1%; Pred. No. 3.2e-58;
Matches 319; Conservative 186; Mismatches 469; Indels 163; Gaps 43;

QY 25 PQVALMKTADELGEIFKFEAPGVRVTRYLSSORBLIKEACDESFRDNLSOALKFVRDFAGD 84
Db 63 PHLSTKLSQQYGDVLIQIRIGSTPVVLSGLNTIKQA-----LVKQGDGDFKGR 110
QY 85 GLFTSWTHEKN-----WKKAHNILLPSFSQOAMKY-----HA 117
Db 111 PLYSFTLIANGQSMFNPDSGPLWAARRL-----AQNALASFISIADPTLASSCYLEE 165
QY 118 MMVDIAVOLVOKWERLNAD-EHIEVPEDMTRTLDTIGLCGFNYRFSFYRDOHPHFTTS 176
Db 166 HVSKEAEYLSIKFOLMAEVGHFDPFKLVSVANVICAICFGRYD--HDDQELLSIVN 223
QY 177 MYRALDEAMNK-----LQRANDP--DPAYDENKRFQFQEDIKVMDLVDKIIADRKA 225
Db 224 LSNEFGEVTGTCYPADFIPLRYLPSNLSLDAFKLNKKFY-----SFMKKLKEHYR 275
QY 226 SEQ-----SDDLTHMLNGK-DPETGEPLDENIRYQIITFLIAGHETTSGLLSFALY 278
Db 276 TFEKHGIRDITSLIEHCODRLDENANVOLSDDKVITIVDFLFGAGDPTITTAISWSLM 335
QY 279 FLVKNPHVLQKAAEAAARVL-VDPVPSYQVKQLKYGVKLVNEALRLMPTAPAFSL--YA 335
Db 336 YLVNTPRIQKIQEELDTVIGRDRPRLSDRPQLPYLEAFLETFRHSSFPV-FTIPHST 394
QY 336 KEDTVLGGVEPLEKDELAVLIPOLHRDXTICGDVEEPRPERFENPS-AIQHAFKP-- 392
Db 395 IRDTSUNGFY-IPKGHCVFVQVQVNDHDELWGP-NEFRPERFLTSSGTLDKHLSEKVI 452
QY 393 -FGNGRACIGQOFALHEATLVLMMLKHDFEDHTNYELDIKET--LTLKP---EGFVV 446
Db 453 LFGLRKRCIGETIGRLEVFLEFLAILLQOOMEENVSPGKVDMTTPAYGLTLKHARCEHFQV 512
QY 447 KAKSK-----KIPLGIPSPSTEQS-AKVRKAENAHNTPLLVLYGSNMGTAEGTA 497
Db 513 QMRSSGPRASAAARMIQTAPPVKESSEFVKMKKTGRN-----IIVFYGSQTGAEEFA 567
QY 498 RDLADIAMSKGFAPOVATLDH-----AGNLPR--EGAVLIVTASY-NGHPPDNKQFVDM 550
Db 568 NLSKDAHRYGMRGMSADPEEDLADLSLPEIDKSLVFCMATYEGEDPTNAQDFYDM 627
QY 551 LQOASADEVKGVYSVFGCGDKNWTYQKVP-----FIDETLAAGAENIADRGADAD 607
Db 628 LQETDVD-LTGKFAVFLGNK-----TYEHENAMKGYVDORLEQLGAQRIEFLGLGDDG 682
QY 608 DREGTYEWEHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMH----- 659
Db 683 NLEEDFITWREQFPAVCEFFGVEATGEESIRQVELVYHE---DMDVAKVYTGEMGRK 739
QY 660 -----GAFSTNVASKELQOPGASRSTRHLEIEL-PKEASYOEGDHLGVIPIRN 706
Db 740 SYENQKPPFDKPNFLAAVTANRKLQ-GTERHLMHLELSDSKIRYESGDHVAVYIPAN 798

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:12 ; Search time 18 seconds
(without alignments)
1713.068 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKENPQPTFGELKNLPL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705.5	12.9	588	4	US-09-627-216A-14
2	678	12.4	1429	1	US-07-642-002-2
3	678	12.4	1429	2	US-08-365-486A-13
4	678	12.4	1429	2	US-08-319-866-11
5	678	12.4	1429	2	US-08-880-342-13
6	678	12.4	1430	2	US-08-705-625-4
7	678	12.4	1430	3	US-09-010-998-5
8	678	12.4	1430	4	US-09-220-574-4
9	675	12.4	1433	2	US-08-365-486A-21
10	675	12.4	1433	4	US-09-123-708-4
11	675	12.4	1433	4	US-09-123-624-3
12	675	12.4	1433	4	US-08-880-342-21
13	675	12.4	1434	2	US-08-365-486A-19
14	675	12.4	1434	4	US-08-880-342-19
15	675	12.4	1554	2	US-08-705-625-3
16	675	12.4	1554	3	US-09-010-998-6
17	675	12.4	1554	4	US-09-220-574-3
18	665.5	12.2	1144	1	US-08-147-812-5
19	665.5	12.2	1144	2	US-08-319-866-12
20	664.5	12.2	1144	4	US-09-123-708-2
21	664.5	12.2	1144	4	US-09-123-624-2
22	662	12.1	1146	4	US-09-126-109-12
23	654.5	12.0	693	1	US-08-553-279-2
24	650	11.9	1153	1	US-08-314-917-2
25	650	11.9	1153	1	US-08-265-046-2
26	650	11.9	1153	2	US-08-465-522-2
27	650	11.9	1153	5	PCT-US93-11401-2

28	650	11.9	1153	5	PCT-US95-07849-2	Sequence 2, Appli
29	599.5	11.0	1205	2	US-08-319-866-10	Sequence 10, Appl
30	599.5	11.0	1205	4	US-09-123-708-6	Sequence 6, Appli
31	599.5	11.0	1205	4	US-09-123-624-6	Sequence 2, Appli
32	598.5	11.0	1205	1	US-07-908-245-2	Sequence 83, Appl
33	597	10.9	679	4	US-09-302-620B-83	Sequence 4394, Ap
34	593	10.9	679	4	US-09-134-001C-4394	Sequence 9, Appli
35	583.5	10.7	629	4	US-08-319-866-9	Sequence 16, Appl
36	564.5	10.3	1350	2	US-08-948-564-16	Sequence 98, Appl
37	460	8.4	576	3	US-09-302-620B-98	Sequence 99, Appl
38	391.5	7.2	540	4	US-09-302-620B-99	Sequence 25, Appl
39	383.5	7.0	540	4	US-08-457-274A-25	Sequence 2, Appli
40	378.5	6.9	504	1	PCT-US95-05758-25	Sequence 2, Appli
41	378.5	6.8	504	5	US-09-144-367-2	Sequence 97, Appl
42	370.5	6.8	503	4	US-09-302-620B-97	Sequence 102, App
43	352	6.5	522	4	US-09-302-620B-102	Sequence 96, Appl
44	349	6.4	512	4	US-09-302-620B-96	
45	349	6.4	522	4	US-09-302-620B-96	

ALIGNMENTS

RESULT 1

US-09-627-216A-14
; Sequence 14, Application US/09627216A
; Patent No. 6368837
; GENERAL INFORMATION:
; APPLICANT: Sariasiani, Sima F
; APPLICANT: Tang, Xiao-Song
; APPLICANT: Qi, Wei Wei
; APPLICANT: Vannelli, Todd
; APPLICANT: Gatenby, Anthony
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
; FILE REFERENCE: BCI009 US NA
; CURRENT APPLICATION NUMBER: US/09/627,216A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-09-627-216A-14

Query Match	12.9%	Score	705.5	DB	4	Length	588
Best Local Similarity	31.9%	Pred. No.	2.1e-53				
Matches	189	Conservative	92	Mismatches	245	Indels	67
Gaps	19						
QY	499	DLADIAMKGFAPQVATFLDSHAGNLPRGAVLIIVTASY-NHPPDPNNAKQFVDWLDQASAD	557				
Db	18	DLDYYA-----ADDEYAEKFKETFAFFFLATYGDGPTDNNARYKWFTEG----	65				
QY	558	EYKGV-----RYSVFGCGDKNWTYQKVPAFIDETLAAKGAENIADRGADASDDPEGT	612				
Db	66	DDRGVWLEKLYHGVFGLGNKQY-EHFNKIALVWDEGLTEQCAKRFVPVGLGDDDDQSDIEDD	124				
QY	613	YESWREHMSDVAAAYFNLDIENSEDNKS-----TSLT-----QFVDSAADMPL	655				
Db	125	FSAWKELWPELDOLL-LD-----EDDKTAATPYTAAPYRVVHFHDKPDTFSENHSOTNG	179				
QY	656	AKMHA-----FSTNVASKELQPCQSARSTRHLELTPKEA-SYOEGLHGVIPRNYEGIV	711				
Db	180	HTVHDQHPCRSNVAVKKELHTPESDRSCHLEFEDISHGLSVETGHDVGVYCNLEVV	239				
QY	712	NRVTARFGLDASQOIRLEAEKEEKLHL-----PLAKTVSVEELQYVELQDPVTRTQL	764				
Db	240	EEAEKLGILPDTYFSLHIDNEDGTPLGGFTLQPPPPCTLRKALTNYADLLSSPKKSTL	299				
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Db 300 LALAAHASDATEADRIQLFASREGKDEYAEWIVANQORSLLVEAPPSAKPPLGVFFAAI 359
QY 821 LPSIRPRYSISSPRVDEKQASITVSVSGAWSGYGEVKGASNY-----LAEQEG 874
Db 360 APRLQPRYSISSPKVNRHIVTCALYV-EKTPGGRHKGICSTWKNMNAVPLTENQDC 418
QY 875 DTITCFISTPQSEFTLPKDPETPLIMVPGCTGVAPFRGVQARKQLKEQOQSLGEAHLVF 934
Db 419 SSAPFVRT--SNFRLPADPKVPVIMIGPGTGLAPRGLQERLALKESGTELQGSILFF 476
QY 935 GCRSPHEDLYQBELENAOSEGIIT-LHTAFSRMPNPKTYVQHVQMEQDGKLIELLDG 993
Db 477 GCRNRKVDYFENELNFFENGALSSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG 535
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLOOLEEKGRYAKDVW 1046
Db 536 AYLIVCGDAKMAKDVHRLTHIVQEGNLDSSKAELYVKNLQMSGRYLRDVW 588

RESULT 2
US-07-642-002-2
; Sequence 2, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Brett, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,002.
; FILING DATE: 19910118
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.033576
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 296-5500
; TELEFAX: (202) 296-7830
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-642-002-2

Query Match 12.4%; Score 678; DB 1; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPSTQSAKVKRAE-----NAHTYPLLVYGSNMGTAEGTARDIADIA 504
Db 718 GTNGPTTKRATGFRKLAEAVEKFAKSLMGQAMAKRVATILYATETGKSAVAKTICEIF 777
QY 505 MSKGPAFQATDSDHAGNLPRGAVLIVTASY-NGHPPDNAOF----- 547
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Db 894 AFGHADVTLLEELGGERILKMRGDBLCGQEEAFRTWAKKFKAAKADVFCVGDVNIIEKP 953
QY 638 NKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQPGSGARSSTR 682
Db 954 NNSLISNDRSWKRNKFRITYVAEPDLTQGLSNVHKRVSAARLLSRQLQSPKFSRSTI 1013
QY 683 HLEIEL--PKEASYQEGDHLGVIPIRNYEGIVNRVTARF--GLDASQOIRLEAEEELLAHL 738
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QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHVKVELEALLE-KO 787
Db 1074 GVISNWKDESRLPCTIFQAIFYLDITTPPTPLQQLQFASLATNEKEKQRLVLSKGLQ 1133
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLSIRPRYSISSPRVDEKQASITVS 847
Db 1134 EYEEWKWGNPTMVEVLEEFPSIQMPATLLLTQLSLQPRYSISSPPDMPDEVLHTVA 1193
QY 848 VVSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVPGTG 906
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QY 907 VAPFRGFQVARK-QLKEQOQSLGEAHLVFCGRSPHEDYLYQBELENAQSEGII-TLHTAF 964
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QY 965 SRMPNPKTYVQHVQMEQDGKLI--ELLQGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022
Db 1313 SREPRPKYQDVQLQEAESVYRALKEQGGHIVCGDVTMAADVKA-IGRIMTQOQK 1371
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046
Db 1372 LSEEDAGVFSRLRDNRYHEDIF.1395

RESULT 3
US-08-365-486A-13
; Sequence 13, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
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Db 1194 IVSYHTRDGEVPHHVCSSWLNRIQADDDVPCFVRGAPS-FHLPNPOVPCILVPGGTG 1252
QY 907 VAPFRGCVQARK-OLKEQOSLGEAHLVFCGRSPHEDYLYQLELENAQSEGII-TLHTAF 964
Db 1253 IAPFRSFWOORFDIOHKGMPVLMVLFVFCGRSQKIDHIIYREETLQAKNGVFRILYAT 1312
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLDOGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022
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QY 1023 VSEADARLWLOOLEKGRYAKDVW 1046
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RESULT 5

US-08-880-342-13
; Sequence 13, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-13

Query Match 12.4%; Score 678; DB 4; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLVLYGSNMGTAEGTARDIADIA 504
Db 718 GTNGTPTKRAIGFKKLAEVKFSAKLMQAMAKRVKATILYATETGSKSQAAYKTLCIEIF 777

QY 505 MSKGFAPOAVTLDSSHAGNLPREGAVLIVTASY-NGHPPDNAKOF----- 547
Db 778 KHAFDAKAMSMEYDIIVHLEHEALVIVTSTFGNGDPPENGKFCGALMEMRHPNSVQEE 837
QY 548 -----VDWLQD-ASADEVKGVRYSVFCGCDKNWATTYQKVP 582
Db 838 RKSYKVRNFSVSSDSRKSQDGPDLRDNFESTGFLANVRFVSFGLGSR-----AYPHC 893
QY 583 AF---IDETLAAGAENIADRGADASDDFEGTYEWEHMHMSDVAAYENL--DIENSED 637
Db 894 AFGHAVDTLLEELGGERILKMRGDELQGOEAFRTWAKKVFKAACDVCVGDVNIERP 953
QY 638 NKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSAARSTR 682
Db 954 NNSLISNDRSWMKRNKFLTYVAEPDLTQGLSNVHKRVSAARLLSRNLQSPKPSRSII 1013
QY 683 HLEIEL--PKEASYQEGDHLGVIPIRNYEGIVNRVTRF--GLDASQOIRLEAEKEKLAHL 738
Db 1014 FVRLHTNGNQLQYQGDHLGVFPGNHEDLVNALTIERLEDAPPANHVVKVEMLEERTAL 1073
QY 739 PLAKTVSYEELL-----QYVELQDPVTRTOLRAMAAKTVCPPHKEVELEALLE-KQ 787
Db 1074 GVISNWKDESRLPCTIFQAFKYLDITTPPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSFIALPSIRPRYSISSSPRVDEKQASITVS 847
Db 1134 EYEENKWKGNPTMVEVLEFPISQMPATLLTLQLSLQPRYSISSSPDMPYDVEHLTVA 1193
QY 848 VVSGBAWSGYGE-YKGIASNYLAELQEGDTTCFTSTPQSEFTLPKDPPTPLIMVPGGTG 906
Db 1194 IVSYHTRDGEVPHHVCSSWLNRIQADDDVPCFVRGAPS-FHLPNPOVPCILVPGGTG 1252
QY 907 VAPFRGCVQARK-OLKEQOSLGEAHLVFCGRSPHEDYLYQLELENAQSEGII-TLHTAF 964
Db 1253 IAPFRSFWOORFDIOHKGMPVLMVLFVFCGRSQKIDHIIYREETLQAKNGVFRILYAT 1312
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLDOGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022
Db 1313 SREPDPRKYYQDVVLQEQLAESVYRALKEQGGHIVCGDVTMAADVLKA-IQRIWTOQOK 1371
QY 1023 VSEADARLWLOOLEKGRYAKDVW 1046
Db 1372 LSEEDAGVFISRLDDNRYHEDIF 1395

RESULT 6

US-08-705-625-4
; Sequence 4, Application US/08705625
; Patent No. 5908756
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samie R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,625
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57071
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-705-625-4

Query Match 12.4%; Score 678; DB 2; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
QY 457 GIPSPSTQSAKKVRKAE-----NAHNTPLLVYSGNMGTAEGTARDLADIA 504
DB 718 GTNGTPTKRRRAIGFKKLAEEAVKFSAKLMQAMAKRVKATILYATETGKSQAYAKTLCEIF 777
QY 505 MSKFAPQAVATLDSHAGNLPREGAVLIVTASY--NGHPPDNAKQF----- 547
DB 778 KHAFDKAMSMEEYDIVHLEHEALVTVTSTFGNGDPPENGKEFGCALMEMRHPNSVQEE 837
QY 548 -----VDWLDQ--ASADEVKGVRYSVFGCGDKKNWATYQKVP 582
DB 838 RKSXYKVRNVSYSKSSGDPDLRDNFESTGPLANVRFVSFGLGSR----AYPHFC 893
QY 583 AF----IDETLAAGAENIADRGADASDDFGTYEEWREHMSVDAAYFNL--DIENSED 637
DB 894 AFGHAVDTLLEELGERILKMRGDELCCGEEAFTWAKVKVKAACDVCVGDVNVTEKP 953
QY 638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSARSTR 682
DB 954 NNSLISNDRSKRNRKFRITYVAEAPDLTQGLSNVHKRVSAARLLSRONLQSPKFSRSTI 1013
QY 683 HLEIEL--PKEASVOEGDHLGVIIPNVEGIYVNTARF--GLDASQOIRLEAEKEKLAHL 738
DB 1014 FVRLHTNGNQLQOPGDHLGVFPNGNHEDLVNALTIERLEDAPPANHVVKVEMLEERNAL 1073
QY 739 PLAKTVSYEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE--KQ 787
DB 1074 GVISNWKDESRLPCTTFIAFKYILDTTPTPLQLOQFASLATNEKEKQRLVLSKGLQ 1133
QY 788 AYKEQVLAKRLTMLELEKYPACEMKSEFTALLPSIRPRYSISSSPRVDEKQASITVS 847
DB 1134 EYEMWKGKNTMVEVLEFPFSIQMPATLLLTQLSLQPRYSISSSPDMPDEVHLTVA 1193
QY 848 VVSGEANSWGYCE--YKGIASNYLAELOEGDTTTCFTSTPQSEFTLPKQDPTLIMVGGTG 906
DB 1194 IVSTHTRDGEVPVHGVCSWLNRLQADDVVPFCVRGAPS--FHLPRNPQVPCILVPGGTG 1252
QY 907 VAPPRGFVQARK--OLKEQGQSLGEAHLYFGCRSPHEDLYOEELENAQSEGII--TLHTAF 964
DB 1253 IAPRSEFWQQRQEDIQHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGFRLEYTAY 1312
QY 965 SRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHYICGDSQMAPAVEATLMKSYADVHQ 1022
DB 1313 SREPRPKKYVDVLQOLAESVYRALKEQGGHIYVCGDVTMAADVLA--IQRTMTQOGK 1371
QY 1023 VSEADARLWLOOLEEKRYAKDVW 1046
DB 1372 LSEADAGVFIISRLKDDNRIYHEDIF 1395

RESULT 7
US-09-010-998-5
; Sequence 5, Application US/09010998
; Patent No. 6103872

GENERAL INFORMATION:
APPLICANT: Snyder, Solomon
APPLICANT: Jaffrey, Samie
APPLICANT: Snowman, Adele
APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,998
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.73424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6103872e
US-09-010-998-5

Query Match 12.4%; Score 678; DB 3; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
QY 457 GIPSPSTQSAKKVRKAE-----NAHNTPLLVYSGNMGTAEGTARDLADIA 504
DB 718 GTNGTPTKRRRAIGFKKLAEEAVKFSAKLMQAMAKRVKATILYATETGKSQAYAKTLCEIF 777
QY 505 MSKFAPQAVATLDSHAGNLPREGAVLIVTASY--NGHPPDNAKQF----- 547
DB 778 KHAFDKAMSMEEYDIVHLEHEALVTVTSTFGNGDPPENGKEFGCALMEMRHPNSVQEE 837
QY 548 -----VDWLDQ--ASADEVKGVRYSVFGCGDKKNWATYQKVP 582
DB 838 RKSXYKVRNVSYSKSSGDPDLRDNFESTGPLANVRFVSFGLGSR----AYPHFC 893
QY 583 AF----IDETLAAGAENIADRGADASDDFGTYEEWREHMSVDAAYFNL--DIENSED 637
DB 894 AFGHAVDTLLEELGERILKMRGDELCCGEEAFTWAKVKVKAACDVCVGDVNVTEKP 953
QY 638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSARSTR 682
DB 954 NNSLISNDRSKRNRKFRITYVAEAPDLTQGLSNVHKRVSAARLLSRONLQSPKFSRSTI 1013
QY 683 HLEIEL--PKEASVOEGDHLGVIIPNVEGIYVNTARF--GLDASQOIRLEAEKEKLAHL 738
DB 1014 FVRLHTNGNQLQOPGDHLGVFPNGNHEDLVNALTIERLEDAPPANHVVKVEMLEERNAL 1073

QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKTVCPHPKVELEALLE-KQ 787
Db 1074 GVISNWKDESRLPPCTIFQAFKYYLDITPTPTLQLOQFASLATNEKEKORLLVLSKGLQ 1133
QY 788 AYKEQVLAKRLTLMLELLEKYPACEMKFEFIALLPRIYRYSISSPRVDEKQASITVS 847
Db 1134 EYEEKWKGNPTMVELEFPSTQMPATLLLTQSLQPRYYSISSSPDMYPDEVHLTVA 1193
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPPTPLIMVGPVG 906
Db 1194 IVSYHTRDGEVPHHGVCSWLNRIQADDDVPCFVRGAPS-FHLPNRPQVPCILVGPVG 1252
QY 907 VAPFRGEVQARK-OLKEQOGSLGEAHLFYFCRSPHEDYLYOELENAQSEGII-TLHTAF 964
Db 1253 IAPFRSFQORQFDIHKGMNCPMVLVEGCRQSKIDHIYRETLQAKNKGVRFLYTAY 1312
QY 965 SRMPNPKTYVQVHMEQDGKKLI--ELLQOGAIFYICGDSQMAVAEATLMKSYADVHQ 1022
Db 1313 SREPDPRKPYQDVQLQELAEYSYRALKEQGGHYYVCGDVTMAADVILKA-IQRIIMTQOGK 1371
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046
Db 1372 LSEEDAGVFISRLDDNRHEDIF 1395

RESULT 8

US-09-220-574-4
; Sequence 4, Application US/09220574
; Patent No. 6168926
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samle R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,574
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,625
; FILING DATE: 30-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kegan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.57071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-220-574-4

Query Match 12.4%; Score 678; DB 4; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;

Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGNSMGTAGETARDIADIA 504
Db 718 GNGTPTTKRRATGFKLAEAIVKSAKLMQAMAKRVKATILITATETGKSQAYAKTICEIF 777
QY 505 MSKGFAPQAVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF-----547
Db 778 KHAFDAKAMSMEEDYIVHLEHEALVLTSTFTGNGDPPENGEKFGCALMEMRHPNSVQEE 837
QY 548 -----VDWLQO-ASADEVKGVRYSVFCGCGKNWATTYKQVP 582
Db 838 RKSXYKVRNSVSSYSRKSXSGDGLDRDNFESTGTPLANVRSFVGLGSR----AYPHFC 893
QY 583 AF---IDETLAAGAENIADRGADASDDFECTYEEHREHMSDVAAAYNL--DIENSED 637
Db 894 AFGHAVDTLLELGGRIILKMRGDELCGOEAFRTWAKKVKAAACDVFCVGDGVNIK 953
QY 638 NKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSAARSTR 682
Db 954 NNSLISNDRSKRNKFRLTYYAEAPDLTQGLSNVHKRYSAARLLSRQNLQSPKFSRSTI 1013
QY 683 HLEIEL--PKEASYQEGDHLGVIPRYNEGIVNRTARF--GLDASQOIRLEAEKEKLAHL 738
Db 1014 FVRLHTNGQELQYQPGDHLGVFPNGHEDLVNALIERLEDAPPANHVVKVEMLEERTAL 1073
QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKTVCPHPKVELEALLE-KQ 787
Db 1074 GVISNWKDESRLPPCTIFQAFKYYLDITPTPTLQLOQFASLATNEKEKORLLVLSKGLQ 1133
QY 788 AYKEQVLAKRLTLMLELLEKYPACEMKFEFIALLPRIYRYSISSPRVDEKQASITVS 847
Db 1134 EYEEKWKGNPTMVELEFPSTQMPATLLLTQSLQPRYYSISSSPDMYPDEVHLTVA 1193
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPPTPLIMVGPVG 906
Db 1194 IVSYHTRDGEVPHHGVCSWLNRIQADDDVPCFVRGAPS-FHLPNRPQVPCILVGPVG 1252
QY 907 VAPFRGEVQARK-OLKEQOGSLGEAHLFYFCRSPHEDYLYOELENAQSEGII-TLHTAF 964
Db 1253 IAPFRSFQORQFDIHKGMNCPMVLVEGCRQSKIDHIYRETLQAKNKGVRFLYTAY 1312
QY 965 SRMPNPKTYVQVHMEQDGKKLI--ELLQOGAIFYICGDSQMAVAEATLMKSYADVHQ 1022
Db 1313 SREPDPRKPYQDVQLQELAEYSYRALKEQGGHYYVCGDVTMAADVILKA-IQRIIMTQOGK 1371
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046
Db 1372 LSEEDAGVFISRLDDNRHEDIF 1395

RESULT 9

US-08-365-486A-21
; Sequence 21, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/365,486A
: FILING DATE: 23-DEC-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 8255-0018
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1433 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-365-486A-21

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Query Match 12.4%; Score 675; DB 2; Length 1433;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY	457	GIPSPTEQSAQKVRKAE-----NAHNTPLLVLYSGNMGTAGCTARDLADIA	504
Db	722	GTNGTPTTKRAIGFKKLAAEAVKFSAKLMGQAMAKRVKATILYATETKSOAYAKTCEI-	780
QY	505	MSKGFAPOQVATLDSH-AGNLPREGAVLIVTASV-NGHPDNDAKOF-----	547
Db	781	FKHAFDAKVMSEEDYDVLHEHETLVLTIVTSTFGNGDPPENGEKFGCALMEMRHPNSVQE	840
QY	548	-----VDWLQD--ASADEVKGVRYSVFGCGDKNNWATTYQKV	581
Db	841	ERKSYKVRNFSVSSYSDSQSSGDGPDLDNFBSAGPLANVRFSVFGLSGR-----AYPHF	896
QY	582	PAR---IDENLAAGAENIADREADAASDDFEGTYEWRHMSDVAAYENL--DIENSE	636
Db	897	CARGHAVDTLLELGGERILKMEGEDLCOGEAFRTWAKVKFAACDVFCVGDDVYNIK	956
QY	637	DNKSTJLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSARST	681
Db	957	ANNSLISNDSRWKRNFRLTFAVAEAPELTQGLSNVHKRYVSAARLLSRQLQSPKSSRST	1016
QY	682	RHLEIEL--PKEASYQEGDHLGVIPRYNEGIVNRVTRAFGLDA--SQOIRLBAEREK--	734
Db	1017	IFVRLHTNGSQELQYQGDHLGVFPGNHEDLVNVALTERLE-DAPPVQMWKVLELEGRNT	1075
QY	735	-----LAHLPLAKTVSVEELLQVYVELQDPVTRTQLRAMAAKTVPCHKVELEALLE-	785
Db	1076	ALGVISNWTDELRLPCTIFQAPKYYLDITPTPTLQLOQFASLATESEKQRLLVLVLSKG	1135
QY	786	KQAYKEQVLAKRULMLELLEKYPACEMKFEFTALLPSIRPRYYSISSSPRVDEKQASIT	845
Db	1136	LQYEEWKWCKNTIIEVLEEFYSIQPATLITLQSLQPRYISSSSDDPMDPEVHLT	1195
QY	846	VSVVSGEAMSGYGE-YKGIASNYLAELOEGDTITCFISTPQSEFTLPKDPETPLIMVGP	904
Db	1196	VAIVSYRTRDGEPIHHGVCSWLNRIOADELVPFCFVRGAPS-FHLPNRNPQVPCILVGP	1254
QY	905	TGVAPPRGFFVOAK-QLKEQGOSLGEAHLYFGCRSPHEDLYQBELENAQSEGI--TLHT	962
Db	1255	TGTAPEFRSFQWQHFQDIHQKGMPCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT	1314
QY	963	AFSRMPNQPTYYQHVYQOQGGKLI--ELLDQGAHFYICGDGOMAPAVENATLMKSYADV	1020
Db	1315	AYSREPDKPKKYQDILLOEALAESVYPALEQGGHYVCGDVTMAADVLA-QIRINTQO	1373
QY	1021	HQVSEADARLWLOOLEKGKYADWV	1046
Db	1374	GKLSAEDAGVYFISMRDDNYHEDIF	1399

RESULT 10

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US-09-123-708-4
; Sequence 4, Application US/09123708
; Patent NO. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-4

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Query Match	12.43;	Score 675;	DB 4;	Length 1433;
Best Local Similarity	28.0%;	Pred. No. 4.9e-50;		
Matches	192;	Conservative 132;	Mismatches 258;	Indels 104; Gaps 23;
Qy	457	GIPSPSTEQSAKKYKKAEE-----NAHTPLLVLYGSMGTAGETARDLADIA	504	
Db	722	GTNGTPTKRAIGFKLAEEAVKFSAKLMGQAMAKRVKATILYATETCKSQAYAKTLCIEI-	780	
Qy	505	MSKFAFQVATLDSH-AGNLPREGAVLIVTASY-NGHPDDNAKOF-----	547	
Db	781	FKHAFDAKVMSEEDIVHLEHETVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQE	840	
Qy	548	-----VDWLDO--ASADEVKGVYRVSVFGCGDKNWTATYQKV	581	
Db	841	ERKSYKVRFNSVSSYSDSQSSGDGPDLLRDNFESAGPLANVRFVFGLSR- ---AYPHF	896	
Qy	582	PAF---IDETLAAGAENIADRGADASDDPEGTYEERHMSDSVAAYFNL--DIENSE	636	
Db	897	CAFCHAVDTLLEELGGERILKMRGDELCGQEEAFRTWAKVKVFAACDVCVCGDDVNIKE	956	
Qy	637	DNKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQGCSARST	681	
Db	957	ANNSLINDRSWKKNKFRLTVEABEPLTOGLSNVHKRVSAARLLSQNSQPKSRKST	1016	
Qy	682	RHLSTEL--PKEASYQEGDHLGVIPRVNVEGVNVRTARFGLDA---SQOIRLEAEERK--	734	
Db	1017	IFVRLHTNGSQELQYQPGDHLGVFPNGHEDLVNALIERLE--DAPPVNQMVKVELLEERT	1075	
Qy	735	-----LAHLPLAKTVSVSEELQYVELQDPVTRTQLRMAAKTVCPHPKVELLEAL-	785	
Db	1076	ALGVISNWTDELRLPCTTFOAKVXYLDITTPPTPLQLQOPASLATSEKEQRLLVLSKG	1135	
Qy	786	KQAYKEQVLAKRLMELLEKYPACEMKFSFIALLPISRPYVSISSSPRVDEKQASIT	845	
Db	1136	LQYEEMKWKGNPTIVELEFPSSQMPATLLLTQLSLQLPYRYSISSSPDMPYDEVHLT	1195	
Qy	846	VSVYSGEAWSCYGE-YKGIASNYLAELQEGDTITCF1STPOSETLPKDPETPLMWGPG	904	
Db	1196	VAIYVSYRTRDGEPIHHGVCSWLNRIQADELVPCFVRGAPS-FHLPNNQPVPCILVWGP	1254	
Qy	905	TGVAPFFGVQARK-OLKEGOSOLGEAHLVYGRCSPHEDYLYQEELENAQSEGII-TLHT	962	
Db	1255	TGIAPFRSFWOORFDLQHKGNPCPMVLVFGCRQSKIDHIIRETLOAKNKGVRELIT	1314	
Qy	963	AFSRMPNQPTIYQVHMVEQDGKKLI--ELLDQGAHFYICGDSGQMAFAVEATLMKSYADV	1020	
Db	1315	AYSEPKPKYVQDILQEQALAESVYRALKEGGHIYVCGDVTWAAADVKA-IQIRMTQQ	1373	
Qy	1021	HQVSEADARLWLOOLEEKGRYAKDWW	1046	

Db 1374 GKLSAEDAGVFISMRDDNRYHEDIF 1399

RESULT 11

US-09-123-624-4

; Sequence 4, Application US/09123624

; Patent No. 6149936

; GENERAL INFORMATION:

; APPLICANT: SCHRADER, Jurgen

; APPLICANT: CODECKE, Axel

; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

; FILE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

; FILE REFERENCE: 511169-2004

; CURRENT APPLICATION NUMBER: US/09/123,624

; CURRENT FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: 08/553,503

; PRIOR FILING DATE: 1996-03-01

; PRIOR APPLICATION NUMBER: 4411402.8

; PRIOR FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 4

; LENGTH: 1433

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-123-624-4

Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSMGTAGTARDIADIA 504

Db 722 GTNGTPTKRAIGFKLAFAVSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCI- 780

QY 505 MSKGPAPQATLDH-AGNLPREGAVLIVTASY-NGHPPDPAKQF-----547

Db 781 FKHAFDAKVMSEEDYDIVHLEHTLVVYTFSTFGNGDPPENGEKFCALMEMRHPNSVOE 840

QY 548 -----VDLQDQ-ASADEVKGVRYSVFGCGDKNWTATYQKV 581

Db 841 ERKSKYVRNVSYSYSDSKSGDGDPLDRDNFESAGPLANVRFSVFGLSR-----AYPHF 896

QY 582 PAF---IDETLAAGKAGNIADREASDDFEGTYEENREHMSDVAAYFNL--DIENSE 636

Db 897 CAFGHAVDTLLEELGGERILKMRGDELQGEAEFTWAKVKYKACDVCVCGDDVNIK 956

QY 637 DNKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOQSARST 681

Db 957 ANNSLISNDRSWKRNKFRITFAEAPELTQGLSNVHKRVSAARLLSRONLQSPKSSRST 1016

QY 682 RIULETEL--PKASYOEGDHGIVPRNVEGIVNRYVAREGLDA---SQQIRLEAEEEK-- 734

Db 1017 IFVRLHTNGSQELQVQPGHGVFGNHDHLYNALIERLE-DAPPVNMVKVYVLEERNT 1075

QY 735 -----LAHLPLAKTVSVEELQVLEQDPVTRTQLRAMAAKTVCPKHKVELEALLE- 785

Db 1076 ALGVISNWTDELRLPPCTTIFQAFKYVLDITPTPTPLQVQFASLATSEKEKQRLVLVSKG 1135

QY 786 KQAYEQLVAKRLTLMLELLEKYPACEMKFSEFIALLPSTIRPYYSISSPRVDEKQASIT 845

Db 1136 LQEYEWKMGKNPTIVEVLEEPSIOMPATLLTLQSLLOPRYYSISSPDMYPDEVHLT 1195

QY 846 VSVVSGEAWSGYGE-YKGIASNYLAELQEGDITCFISTPQSEFTLPKDPETPLIMVGP 904

Db 1196 VAIVSYRFDGEGPHHGVCSSWLNRIQADELVPCFVRGAPS-FHLPRNPQVPCILVGG 1254

QY 905 TGVAFRGVQARK-OLKEQOGSLGEAHLFYGCRSPHEDYLYOELENAQSGII-TLHT 962

Db 1255 TGIAPFRSFWQORQFQIOHKGMPVMLVFCRQSKIDHIVREETLQAKNKGVPRELYT 1314

QY 963 AFSRPNQPKTYVQHVMEQDGKKLI--ELLDOGAHFYICGDSQMAPAVEATLMKSYADV 1020

1315 AYSREPDPKYVQDILQFLAESVYRKALKEQGGHIYVCGDVTMAADVLKA-IQRIWTOQ 1373

1021 HOVSEADARLWLQOLEEKGRYAKDVW 1046

1374 GKLSAEDAGVFISMRDDNRYHEDIF 1399

RESULT 12

US-08-880-342-21

; Sequence 21, Application US/08880342

; Patent No. 6218179

; GENERAL INFORMATION:

; APPLICANT: Webster, Keith A.

; APPLICANT: Bishopric, Nanette H.

; APPLICANT: Murphy, Brian

; APPLICANT: Laderoute, Keith R.

; APPLICANT: Green, Christopher J.

; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

; TITLE OF INVENTION: Therapeutic Constructs

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/880,342

; FILING DATE: 23-JUN-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/IB95/00996

; FILING DATE: 13-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/365,486

; FILING DATE: 23-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 8255-0018.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1433 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-880-342-21

Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSMGTAGTARDIADIA 504

Db 722 GTNGTPTKRAIGFKLAFAVSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCI- 780

QY 505 MSKGPAPQATLDH-AGNLPREGAVLIVTASY-NGHPPDPAKQF-----547

Db 781 FKHAFDAKVMSEEDYDIVHLEHTLVVYTFSTFGNGDPPENGEKFCALMEMRHPNSVOE 840

QY 548 -----VDLQDQ-ASADEVKGVRYSVFGCGDKNWTATYQKV 581

Db 841 ERKSKYVRNVSYSYSDSKSGDGDPLDRDNFESAGPLANVRFSVFGLSR-----AYPHF 896

[illegible]

RESULT 13

US-08-365-486A-19
Sequence 19, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructions
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 825S-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-19

Query Match      12.4%; Score 675; DB 2; Length 1434;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY 457 GIPSPSTEQSAKVRKKAEE-----NAHTPLLVLYGSMGTAEGTARDLADIA 504
Db 723 GTNGTPTKRAIGFKKLAAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCEI- 781
QY 505 MSKGFAPOVATLDH-AGNLPREGAVLIVTASY-NGHPPDNAQOF-----547
Db 782 FKAFDAKVMSEEDIVLHLEHTLVLVVTSITFGNGDPPENGKFGCALMEMRHPNSVQE 841
QY 548 -----VDWLDO-ASADEVKGVGVSVFGCGDKNNWATTYQKV 581
Db 842 ERKSYKVRNSVSYSYSDSQSSGDGPDLRDNFESAGPLANVRFSVFLGSR-----AYPHF 897
QY 582 PAR---IDENLAAKGAENIADREADASDDFETYEWRHEHMSDVAAYENL--DIENSE 636
Db 898 CARGHAVDTLLELGERILKMRGDEBLQCEAEAFRTWAKRVKAACDVFCVGDDVNIK 957
QY 637 DNKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNNVAVSKELQPGSGARS 681
Db 958 ANNSLISNDRSKRNKFRFLTFAEAPELTQGLSNVHKRVYSAARLLSRQLQSPKSSRST 1017
QY 682 RHLIEL--PKASYQEGDHLGVIPRNYEGIVNRVYARFGLDA---SQQIRLEAEEBK-- 734
Db 1018 IFVRLHTNGSQEIQYQPDGHLGVFPFGNHEDLVNALLERLE-DAPPVNMQYKVELLEBRNT 1076
QY 735 -----LAHLPLAKTVSYEELLYQYELQDPVYRTQLRAMAKTVCPPHKVELEALLE- 785
Db 1077 ALGVISNWTDELRLPCTIFQAFKYKYLDTTPTPLQLQFASLATSEKEKQRLLVLSKG 1136
QY 786 QYAKEQVLAKRITMLLEKKYACEMKFEFTALLPSIRPRYSISSSPRVDEKQASIT 845
Db 1137 LQYEWKWKGNPTTIVEVLEEFFSIQMPATLLTQLSLQAPRYSISSSPMDYPDEVHLT 1196
QY 846 VSVVSGEAWSGYGE-YKGIASNTYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGP 904
Db 1197 VAIVSYTRDGE GPIHHGVCSWNLRLQADELVPCFVRGAPS-FHLPRNQVPCILLVGP 1255
QY 905 TGVAFFPGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDLYQBELENASQEGII-TLHT 962
Db 1256 TGTAFFRSFQWQRQFDIQHKGMPNCPMVLVFGCRQSRKIDHIYREBTLQAKNKGVFRELYT 1315
QY 963 AFSRMPNPNQTYVQHYVMEODGKKLI--ELLQDGAHFHYGCGSGOMAPAVATLWKSADV 1020
Db 1316 AYSREPDKPKYYQDILLOELQALRSYVYRALKEQGHHYVCGDVTMAADVKA-IQRIMTQ 1374
QY 1021 HQVSEADARLWLOOLEEKGRYAKDVW 1046
Db 1375 GKLSAEDAGYFISMRDDNRYHEDIF 1400

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RESULT 14

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US-08-880-342-19
: Sequence 19, Application US/08880342
: Patent No. 6218179
: GENERAL INFORMATION:
: APPLICANT: Webster, Keith A.
: APPLICANT: Bishopric, Nanette H.
: APPLICANT: Murphy, Brian
: APPLICANT: Laderoute, Keith R.
: APPLICANT: Green, Christopher J.
: TITLE OF INVENTION: Tissue Spec
: TITLE OF INVENTION: Therapeutic
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Dellinger & Associat

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/ STREET: 350 Cambridge Avenue, Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ FILING DATE: 23-JUN-1997
/ APPLICATION NUMBER: US/08/880,342
/ CLASSIFICATION: 514
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IB95/00996
/ FILING DATE: 13-NOV-1995
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/365,486
/ FILING DATE: 23-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sholtz, Charles K.
/ REGISTRATION NUMBER: 38,615
/ REFERENCE/DOCKET NUMBER: 8255-0018.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1434 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-880-342-19
/
/ Query Match 12.4%; Score 675; DB 4; Length 1434;
/ Best Local Similarity 28.0%; Pred. No. 4.9e-50;
/ Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;
/
/ QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSGNMGTAEGTARDIADIA 504
/ DB 723 GINGPTKRRRAIGFKKLAFAVSAKLMQMAKRVKATILYATETGKSOAYAKTICEI- 781
/
/ QY 505 MSKGFAQVATLDH-AGNLPREGAVLIVTASY-NGHPPDNAKQF-----547
/ DB 782 FKHAFDAKVMSEEDYIVHLEHTLVVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQE 841
/
/ QY 548 -----VDWLDQ-ASADEVKGVRYSVFGCGDKKNWATYQKV 581
/ DB 842 ERKSKYKVRNFSVSSYSDSQSGDGPDLRDNFESAGPLANVRFSVFLGSR----AYPHF 897
/
/ QY 582 PAF---IDETLAAGAENTADRGADSDDFEGTYEWEHMSVDVAAYFNL--DIENSE 636
/ DB 898 CAFGHAVDTLLBELGGERILKMGDELGCQGEAFTWAKVKVKAACDVCVGDVNIK 957
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/ QY 637 DNKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQOQSAKST 681
/ DB 958 ANNLSISNDRSNKRNKFRITFVAEAPELTQGLSNVHKRVSAARLLSRQLQSPKSSRST 1017
/
/ QY 682 RHLETEL--PKEASVQEGDHLGVIPRNYEGIVNRTARGLDA---SQOIRLEAEEK-- 734
/ DB 1018 IFVRLHTNGSQELQVQPGDHLGVFPNGHEDLYNALIERLE-DAPPVNMVKVYELLEERT 1076
/
/ QY 735 -----LAHLPLAKTVSVEELLQVLEQDPVTRTQLRAMAKTVCPHPKVELEALL- 785
/ DB 1077 ALGVISNWTDELRPLPCTIFQAFKYLDITTPPTLQOQFASLATSEKEORLLVLSKG 1136
/
/ QY 786 KOAYKEQVLAKRLTMLELEKYPACEMKFSEFIALLPISIRPRIYSSISSPRYDEKQASIT 845
/ DB 1137 LQEEYEWKGNKPTIVLEVLEFPISIQMPATLLLTQLSLQPRYSSISSSPDMYPDEVHLT 1196
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/ QY 846 VSVVSGEAWGSGE-YKGIASNYLAEQBGDTITCFISTPQSEFTLPKDPETPLIMVPG 904
/ DB 1196
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1197 VAIVSYRTRDGGEGPIHHGVCSWLNRIQADELVPCFVRGAPS-FHLPRNPQVPCILVGP 1255
QY 905 TGVADPRGFVQARK-QLKEQGQSLGEAHLVFCGRSPHEDYLYQEELENAQSGIIL-TLHT 962
DB 1256 TGIAPFRSFQQRQFDIOHKGNPCPMVLFVFCGRSKIDHIYREETLQAKNKGVFRELYT 1315
QY 963 AFSRMPNQPVTYQHVMEQDGKKLI--ELLDQGAHFYICGDSGSQMAPAVEATLMKSYADV 1020
DB 1316 AYSREPDKPKYVQDILQQLAEESVYRAKKEGGHYVCGDVTMAADVLA-IQRIMTQQ 1374
QY 1021 HQVSEADARLWLOOLEEGRYAKDVW 1046
DB 1375 GKLSAEDAGVFISRMDDNRHEDIF 1400
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/ RESULT 15
/ US-08-705-625-3
/ Sequence 3, Application US/08705625
/ Patent No. 5908756
/ GENERAL INFORMATION:
/ APPLICANT: Snyder, Solomon H.
/ TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
/ TITLE OF INVENTION: Oxide Synthase
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Witcoff
/ STREET: 1001 G Street, N.W.
/ CITY: Washington, D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20001-4597
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/705,625
/ FILING DATE: 30-AUG-1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kagan, Sarah A.
/ REGISTRATION NUMBER: 32,141
/ REFERENCE/DOCKET NUMBER: 01107.57071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1554 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus norvegicus
/
/ US-08-705-625-3
/
/ Query Match 12.4%; Score 675; DB 2; Length 1554;
/ Best Local Similarity 28.0%; Pred. No. 5.6e-50;
/ Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;
/
/ QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSGNMGTAEGTARDIADIA 504
/ DB 723 GINGPTKRRRAIGFKKLAFAVSAKLMQMAKRVKATILYATETGKSOAYAKTICEI- 781
/
/ QY 505 MSKGFAQVATLDH-AGNLPREGAVLIVTASY-NGHPPDNAKQF-----547
/ DB 782 FKHAFDAKVMSEEDYIVHLEHTLVVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQE 841
/
/ QY 548 -----VDWLDQ-ASADEVKGVRYSVFGCGDKKNWATYQKV 581
/ DB 842 ERKSKYKVRNFSVSSYSDSQSGDGPDLRDNFESAGPLANVRFSVFLGSR----AYPHF 897
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Qy	582	PAF---	IDETLAAG	ENTAD	CEAD	SAD	DFG	TYE	EH	MW	S	VAA	FNL--	DTENSE	636
Db	898	CAG	HAV	D	T	L	E	E	L	G	E	L	G	E	L
Qy	637	DNK	STLS	-----	LQF	V	D	S	A	D	M	P--	LAK	MH-	681
Db	958	ANNS	L	S	N	D	R	S	K	N	K	F	R	L	T
Qy	682	R	H	E	I	E	L	--	P	K	E	A	S	Y	Q
Db	1018	I	F	V	R	L	T	N	G	S	Q	E	L	Q	Y
Qy	735	-----	LAH	L	P	L	A	K	T	S	V	E	E	L	Q
Db	1077	ALG	V	I	S	N	W	T	D	E	L	R	P	C	T
Qy	786	K	O	A	K	E	O	V	L	A	K	R	T	M	L
Db	1137	L	O	E	Y	E	M	K	W	K	N	P	T	I	V
Qy	846	V	S	V	S	E	A	N	G	S	G	Y	C	E	
Db	1197	V	A	I	S	Y	T	R	D	G	E	G	P	I	H
Qy	905	T	G	V	A	P	R	G	F	V	O	A	R	K	-
Db	1256	T	G	I	A	P	R	S	F	W	Q	R	F	D	I
Qy	963	A	F	S	R	M	N	O	P	K	T	Y	Y	H	V
Db	1316	A	Y	S	R	E	D	P	K	K	Y	V	D	I	L
Qy	1021	H	O	V	S	E	A	D	A	R	L	W	L	O	O
Db	1375	G	K	L	S	A	E	D	A	G	V	F	I	S	R

Search completed: May 29, 2003, 08:22:44
Job time : 24 secs

QY 809 FEGTIEENKREHMWSDVAAAYFNLDIENSEDNKSTLSLQF ---VDSA---ADMPLAKMH-- 639

212	Db	LEEDFTWREQWPVACBHFGEATGBESSIRQYELVVVHTDIAAKYVVMGEMGRLSYEN	271
660	QY	-----GAFSTNVASKELQQPGSARSTRHLEIEL-PKEASVQEGDHLGVIPRNYEG	710
272	Db	QPPDPDKNPFLAAVTTNRKLNQ-GTERHLMHELDISDSKIRYESGDHVAVTYPANDSAL	330
711	QY	VNRVTRAFG--LDASQQIRLEAEKEKLAHLPLAKTYSVEELLOYVELODPVTRTOLRAMA	768
331	Db	VNQLGKILGADLVVMSLNNDESNKHPPOCTSVRTALTYYLDITNP-PRTNLYVEL	389
769	QY	AKTVPCHKVELEALLE-----KQAYKEOVLAKRUTMLELLEKYPACEMKTFSEFIALP	822
390	Db	AQYASEPSEQELLRKMASSGEGEYLISWVVEARRHILAILQDCSPRPDDHCELLP	449
823	QY	SIRPRYISSIONPRYDERQASITVSVSGEAMSGEYKGIASNYL-AELOEGDT-----	876
450	Db	RLQARYSTIASSKVVHPSNVHICAVVVEYETKAGRIN-KGVATNWLRAKEPVGENGCRAL	508
877	QY	TYCFSTTQSEFTLPKDPETPLIMVPGTGVAPRGFVQARKOLKQGGOSLGEAHLFYOC	936
509	Db	VPMEYR--KSQFRLPFKATTPVIMVPGTGVAPFPGFIQERAWLRQOGKEVGETLLYYGC	566
937	QY	RSPHEDYLYQBELENASQEGIIIT-LHTAFSRMPNQPTYVQHVMEODGKKLIELDDQGAH	995
567	Db	RRSDELYLREELAQFHRDGGALTLQNVAFSREQSH-KVYVQHLLKQDREHMLKLTGGAH	625
996	QY	FYICGDSOMAPAVEATLMKSYADHVQVSEADARLWLQLEEKRYAKDVWA	1047
626	Db	IYVCGDARNARDVQNTYDITVABELGAMESHAQVADYIKKLTMTKGRYSLOWDS	677

RESULT 2

US-09-765-873A-14
; Sequence 14, Application US/09765873A

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: Patent NO. US20010053847A1
:
: GENERAL INFORMATION:
: APPLICANT: Tang, Xiao-Song
: TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
: FILE REFERENCE: BC1009 US CIP
: CURRENT APPLICATION NUMBER: US/09/765,873A
: CURRENT FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: US 09/627,216
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: US 60/147,719
: PRIOR FILING DATE: 1999-08-06
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft Office 97
:
: SEQ ID NO 14
: LENGTH: 588
: TYPE: PRT
: ORGANISM: Helianthus tuberosus
: US-09-765-873A-14

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[illegible]

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712 QY 12 NRVTARFGDASQOIRLEAEFEKLAHL-----PLAKTVSVVEELQVVELOQDPVTRTOL 764
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240 Db EEA EKLI GLPADT YFSLHIDNEDGTPGLGPTLQPPFPCTLRKALTNYADLSSPKKSTL 299
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
765 QY 765 RAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTWLELLEKYPACEMKFSEFI-AL 820
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300 Db LALAAHASDATEADRLQFLASREGKDEYAEMIVANQORSLLEYMEAFPSAKPPLGVFFFAI 359
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
821 QY 821 LPSIRPRYISISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNY-----LAELOBG 874
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360 Db APRLOQPRYISISSSPKVPNRHIVTCALVY-EKTEGGRIHKIGICSTWKNNAVPLTENQDC 418
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
875 QY 875 DTITCFISTPOSEFTLPKDPETPLIMVGPGTGVAAPFRGFVQARKOLKEQGQSLGAHLYF 934
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419 Db SSAPFIVRT--SNFRLPADKPVPVIMIGPGTGLAPFRGLQERLALKESGTELQGSILFF 476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
935 QY 935 GCRSPHEDYLQEBLENAQSGIIT-LHTAFSRMPENQPKTYVQHVMEQDGKKLIELLDG 993
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477 Db GCRNRKVDFTIYENELNPNFVENGALSELDMAFSR-EGASKEYVQHKXSKASDIWNMLSEG 535
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994 QY 994 AHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLWLOOLEEGRYAKDYM 1046
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536 Db AYLIVCGDKAGMADVHRTLHTIVQEQGNLSSKAEILVYKNLQMSGRVLRDYM 588
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RESULT 3
US-10-224-249-14
; Sequence 14, Application US/10224249
; Publication No. US20030087867A1
; GENERAL INFORMATION:
; APPLICANT: Vogels, Ronald V.
; APPLICANT: Verlinden, Stefan F.F.
; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing anglogenesis
; FILE REFERENCE: 2183-5233US
; CURRENT APPLICATION NUMBER: US/10/224,249
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: PCI/NL00/00482
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: EP 99202263.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/143,101
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1433
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(1433)
; OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-14

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RESULT 3

US-10-224-249-14
; Sequence 14, Application US/10224249

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: Publication No. US20030087867A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Vegels, Ronald V.
: APPLICANT: Verlinden, Stefan F.F.
:
: TITLE OF INVENTION: Gene therapy for enhancing
:
: FILE REFERENCE: 2183-52330US
:
: CURRENT APPLICATION NUMBER: US/10/224,249
: CURRENT FILING DATE: 2002-08-19
:
: PRIOR APPLICATION NUMBER: PCT/NL00/00482
: PRIOR FILING DATE: 2000-07-07
:
: PRIOR APPLICATION NUMBER: EP 99202363.2
: PRIOR FILING DATE: 1999-07-09
:
: PRIOR APPLICATION NUMBER: US 60/143,101
: PRIOR FILING DATE: 1999-07-09
:
: NUMBER OF SEQ ID NOS: 16
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 14
:
: LENGTH: 1433
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CHAIN
:
: LOCATION: (1)..(1433)
:
: OTHER INFORMATION: Human nitric oxide synthase
:
: US-10-224-249-14

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Query Match	12.4%	Score 675;	DB 9;	Length 1433;
Best local Similarity	28.0%;	Pred. No. 1.2e-40;		
Matches	192;	Conservative 132;	Mismatches 258;	Indels 104; Gaps 23;
QY	457	GIPSPTEQSAKVRKKAEE-----	NAHNTPELLVLYGSMGTGAETARDLADIA	504
DB	722	GTNGTPPKRAIGFKLAEAVKSAKLMGQMAKRVKATILYATETSKSQAYAKTCEI	-	780
QY	505	MSKGFAPOQVATLOSH-AGNLPREGAVLIVTASY-NGHPDPONAKOF-----		547
DB	781	EKHAFDAKVMSEEBYDVLVHEHETLVLVVSTFGNGDPPENGKEFGCALMEMRHPNSVQE	840	
QY	548	-----	-VDWLQ-ASADEVKVGRYSVFCSGDKNWTATYQKV	581
DB	841	ERKSYKVRFNVSYSDSQKSSGDPDLRNFESAGPLANVRFSVFLGSR-----	AYPHF	896
QY	582	PAF---IDETLAAGAEANIADRGADASDDFECTYEWEHRHMSDVAAAYFNL--	DIENSE	636
DB	897	CAGHAYDVTLLLELGGSRILKMRGDESLCQGEAFRTWAKVKFAACDVFVCGDDVNIK	956	


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Db 468 RPTGVVNTLLKNVEIQNKTEKPLVHYDLSGRGKFNKFLPVHVRNSFKLPKNSTT 527
Qy 897 PLIMVPGTGVAPRGFVOARKOLKEQOSLGEAHLFGCRSPHEDYLOEE--LENAOSE 955
Db 528 PVILIGTGVAPLGRFVRVQVQKNGVNGKTLFYGCRNSNEDFLYKQEWAYASVL 587
Qy 956 G-IITLHTAFSRMPNQKTYVQHVMEODGKKLIELLDQGAHFYICGDSQMAPAVEATLM 1014
Db 588 GENFEMENAFSRQPSKVKYVQDKILENSQLVHELLTEGALIYYCGDASRMARDVQTTIS 647
Qy 1015 KSYADVHQVSEADARLMLQLEEKGRYAKDWM 1046
Db 648 KIVAKSREISDKAAELVKSMKVQNRQYQEDVM 679

RESULT 11
US-10-138-916-117
; Sequence 117, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYTOCHROME P450
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; CURRENT FILING DATE: 2002-05-03
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/976,800
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/302,602
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-916-117

Query Match 11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKETITLKPEGFVVVAKSKKI----PLGGIPSPTEQSAKKVKKKAENAHNTPLLYL 485
Db 5 KLDLYVIITLVVAAYAFKNOFLDQPDQDTGFLNTDGSNSRDVLTSLTKNNKNT--LLL 62
Qy 486 YGSNMGTAEGTARDLADTAMSK-GFAPOVATLDSH----AGNLREGAVLIVTASY-NGH 539
Db 63 FGSOTGTAEYDANKLSRELHRSFGLKTMVADFADYDWDNFDGIDITDILVFFVATYGE 122
Qy 540 PPDNAKQFVMDQASADEVKGVRYSVFGCGDKNWTYQKVPF---IDETLAAGAEN 596
Db 123 PTDNADEFHTWLTE-EADTLSTLKYTVFGLGN---STYEFNAIGRKRFRLLSEKGGDR 177
Qy 597 IADRGADASDDFGTVEE-----WREHWSVVAAYFNLD----- 631
Db 178 FAEYAE---GDGTTGLDEDFMAWKNDVFDALKNDLNFEEKELKYEPNVKLTERDDLSAA 234
Qy 632 ---TENSNDKSTLSLOFVSAADWPLAKMHGAFSTNVVASKELQQPCGSARSTRHLEL 688
Db 235 DSQVSLGEPNKKYINSEGIDITK-G-PDHTH-PYLARITETRELFS-SKDRCHLHVEFDI 291
Qy 689 PK-EASYOEGDHLGVIPRNTYEGIVNRVTAFFGLDASQOIRLEABE-EKLAHLPLAKTVSV 746
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Db 292 SESNLKVTGTHLAIWPSNSDENIKQFAKCFGLDKLDTVIELKALDSTYIPPTPTTY 351
Qy 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKHVEALL----EKQAYKEQVLAKRLTML 801
Db 352 GAVIRHLEISGPPVSROFFLSIAG---FAPDEETKKAFTRLGDKQEFPAKVTRKFNIA 408
Qy 802 ELL-----EKYPACEMKFSEFTALLPSIRPRYSISSSPRVDEKQASIFSVSVGEAMSGY 857
Db 409 DALLYSSNNAPWSVDPFEFLIENVPHLTPTPRYSISS--SLSEKQLINVTAVVEAEEDAG 467
Qy 858 GEYKGIASNYLAELQ-----EGDTITCTFISTP-----OSEFTLPKDPET 896
Db 468 RPTGVVNTLLKNVEIQNKTEKPLVHYDLSGRGKFNKFLPVHVRNSFKLPKNSTT 527
Qy 897 PLIMVPGTGVAPRGFVOARKOLKEQOSLGEAHLFGCRSPHEDYLOEE--LENAOSE 955
Db 528 PVILIGTGVAPLGRFVRVQVQKNGVNGKTLFYGCRNSNEDFLYKQEWAYASVL 587
Qy 956 G-IITLHTAFSRMPNQKTYVQHVMEODGKKLIELLDQGAHFYICGDSQMAPAVEATLM 1014
Db 588 GENFEMENAFSRQPSKVKYVQDKILENSQLVHELLTEGALIYYCGDASRMARDVQTTIS 647
Qy 1015 KSYADVHQVSEADARLMLQLEEKGRYAKDWM 1046
Db 648 KIVAKSREISDKAAELVKSMKVQNRQYQEDVM 679

RESULT 12
US-09-976-800-117
; Sequence 117, Application US/09976800
; Publication No. US20030077795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYTOCHROME P450
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-09-976-800-117

Query Match 11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKETITLKPEGFVVVAKSKKI----PLGGIPSPTEQSAKKVKKKAENAHNTPLLYL 485
Db 5 KLDLYVIITLVVAAYAFKNOFLDQPDQDTGFLNTDGSNSRDVLTSLTKNNKNT--LLL 62
Qy 486 YGSNMGTAEGTARDLADTAMSK-GFAPOVATLDSH----AGNLREGAVLIVTASY-NGH 539
Db 63 FGSOTGTAEYDANKLSRELHRSFGLKTMVADFADYDWDNFDGIDITDILVFFVATYGE 122
Qy 540 PPDNAKQFVMDQASADEVKGVRYSVFGCGDKNWTYQKVPF---IDETLAAGAEN 596
Db 123 PTDNADEFHTWLTE-EADTLSTLKYTVFGLGN---STYEFNAIGRKRFRLLSEKGGDR 177
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QY 597 IADRGADASDDFEGTYYY-----WREHMDSVAAAYFNLD----- 631
Db 178 FAEYAE---GDDGTGLDEDFMAWKNDVFDALKNLDFEKEKELKYPNVKLTREDDLSAA 234
QY 632 ---IENSEDNKSTLSQFVDSADMPKAKHGFSTNVVASKELQPGSGARSTRHLEIEL 688
Db 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELF-SKDRHCIHVEFDI 291
QY 689 PK-EASYQEGDHLGVIPRNYEGIVNRVTRARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746
Db 292 SESNLKYYTGDHLAIWPSNSENKQKAFKCGLEDKLDVIELKALDSTYTPFPPIYY 351
QY 747 EELLO-YVELQDPVTRTQIRAMAATVCPHPKVELEALL-----EKQAYKEQVLAKEML 801
Db 352 GAVIRHLEISGVSQRQFFLSIAG---FAPDEETKKAFTRLGGDKQOEFAAKVTRRKNFIA 408
QY 802 ELL---EKYPACEMKFESEFIALPSIRPRYYSISSPRVDEKQASITVSVSGEAWSGY 857
Db 409 DALLYSSNAPWSVDFEFLIENPHLTPIRYYSISS-SLSEKQLINVTAVVEAEEDG 467
QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSETPLPKDPET 896
Db 468 RPYTGVTNLLKLNVEIVQNKTEKPLVHYDLSGPRGKFNKFLPVHVRSRNFKLPKNSYT 527
QY 897 PLIMVPGTGVAPFRGVOARKQKQOSLGEAHLIFGCRSPHEDLYOEE-LENAQSE 955
Db 528 PVILIGTGTGAPLRGFRVRRVQVQKNGVNVGKTLFLFYGRNSNEFLYKQWAEYASVL 587
QY 956 G-IITLHTAFSRMPNPKTYVOHVMEQDGKLELDDOGAHEFYICGDSOMAPAVEATLM 1014
Db 588 GENFEMFASRODPSKVKYVQDKILENSOLVHELLTEGAILIYVCGDSARMARDVQTTIS 647
QY 1015 KSYADVHVQSEADARLWLOOLEKGRYAKDVW 1046
Db 648 KIVAKSREISEDKAELVKSWKQVQRYQEDVW 679

RESULT 13

US-10-138-838-83
; Sequence 83, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,838
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-838-83

Query Match 10.9%; Score 597; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 2.1e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPEGFVYVAKRSKKI-----PLGGIPSPSTBQSARKKVKRKAENAHTLPLVL 485
Db 5 KLDLYVIIITLVAVAAAYFAKQNFLOPQDQPTGFLNTDGSNSRDVLITLAKNKNKT--LLL 62
QY 486 YSNMGTAGTARDLADIAMSK-GFAPQVATLDH-----AGNLPRGAVLIVTASY-NGH 539
Db 63 FGSQTGTAEDYANKLSRELHSRFGTKMTVADFADYDWNDFGDDITDILVFFIVATYGE 122
QY 540 PPDNAKQFVDWLDASADEKGVYRVSVFGCGDKNWTATYQKPAF---IDETLAAGAEN 596
Db 123 PDNADDEFHTWTE-EADTLSTLKYTVFGLGN---STIEFFNAIGRKFDRLLEKGGDR 177
QY 597 IADRGADASDDFEGTYYY-----WREHMDSVAAAYFNLD----- 631
Db 178 FAEYAE---GDDGTGLDEDFMAWKNDVFDALKNLDFEKEKELKYPNVKLTREDDLSAA 234
QY 632 ---IENSEDNKSTLSQFVDSADMPKAKHGFSTNVVASKELQPGSGARSTRHLEIEL 688
Db 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELF-SKDRHCIHVEFDI 291
QY 689 PK-EASYQEGDHLGVIPRNYEGIVNRVTRARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746
Db 292 SESNLKYYTGDHLAIWPSNSENKQKAFKCGLEDKLDVIELKALDSTYTPFPPIYY 351
QY 747 EELLO-YVELQDPVTRTQIRAMAATVCPHPKVELEALL-----EKQAYKEQVLAKEML 801
Db 352 GAVIRHLEISGVSQRQFFLSIAG---FAPDEETKKAFTRLGGDKQOEFAAKVTRRKNFIA 408
QY 802 ELL---EKYPACEMKFESEFIALPSIRPRYYSISSPRVDEKQASITVSVSGEAWSGY 857
Db 409 DALLYSSNAPWSVDFEFLIENPHLTPIRYYSISS-SLSEKQLINVTAVVEAEEDG 467
QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSETPLPKDPET 896
Db 468 RPYTGVTNLLKLNVEIVQNKTEKPLVHYDLSGPRGKFNKFLPVHVRSRNFKLPKNSYT 527
QY 897 PLIMVPGTGVAPFRGVOARKQKQOSLGEAHLIFGCRSPHEDLYOEE-LENAQSE 955
Db 528 PVILIGTGTGAPLRGFRVRRVQVQKNGVNVGKTLFLFYGRNSNEFLYKQWAEYASVL 587
QY 956 G-IITLHTAFSRMPNPKTYVOHVMEQDGKLELDDOGAHEFYICGDSOMAPAVEATLM 1014
Db 588 GENFEMFASRODPSKVKYVQDKILENSOLVHELLTEGAILIYVCGDSARMARDVQTTIS 647
QY 1015 KSYADVHVQSEADARLWLOOLEKGRYAKDVW 1046
Db 648 KIVAKSREISEDKAELVKSWKQVQRYQEDVW 679

RESULT 14

US-10-139-031-83
; Sequence 83, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12

; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
; US-10-139-031-83

Query Match 10.9%; Score 597; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 2.1e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;
QY 430 ELDIKETLTKPEGFYVVKAKSKI-----PLGGIPSPSTEQSAKKVKKKAENAHNTPLLV 485
Db 5 KLDLYIITLVAVAAAFKQFLDQPDGTGFLNTDGSNSRDVLLTLKNNKNT--LLL 62
QY 486 YGSNMGTAEGTARDLADIAMSK--GFAPOVATLDH-----AGNLPREGAVLIVTASY-NGH 539
Db 63 FGSQTGAEDYANKLSRELHSRGLKTMVADFADYDWNFGDITDILVFFIVATYGE 122
QY 540 PPDNAKQFVDWLDQASADEVKGVYVSFGGDKNWTYQKVPF--IDETLAAGAEN 596
Db 123 PTNDAEFHTWLTE--BADTLSTLKYTVFGLGN-----STYEFFNAIGRKFDRLLSEKGGDR 177
QY 597 IADRGADASDDPEGTYEE-----WREHMWSDVAAYFNLD----- 631
Db 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234
QY 632 ---IENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQPGSARSTRHLEIEL 688
Db 235 DSQVSLGEPNKKYINSEGDILTKG--PFDHHT--PYLARITETRELFSS--SKDRHCHIVFE 291
QY 689 PK--EASYQEGDHLGVIPRNVGIVNRTARFGLDASQOIRLEAEE--EKLALHPLAKTVSV 746
Db 292 SESNLAYTTGDHLAIWPSNSDENIKQFAKFCGLEDKLDTVIELKALDSTYTFPPPIY 351
QY 747 EELLQ--YVELQDPVTRTQLRAMAAKTVCPPHKVLEALL-----EKQAYKEQVLAKRUTML 801
Db 352 GAVIRHLEITSGVPSRQFLSIAG---FAPDEETKKAFTRLGGDKQEFKAAKVTTRKFNIA 408
QY 802 ELL---EKPACEMKFESEFIALPSIRPRYYSISSSPRDEKQASITVSVSGEAWSGY 857
Db 409 DALLYSSNAPWSDVPEFLIENVPHLTPRYYSISS--SLSEKQLINVTAVVEAEADG 467
QY 858 GEYKGIASNYLAELQ-----EGDITTCFISPP-----OSEFTLPKDPET 896
Db 468 RPYTGVTNLLKNVEIVQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRNSNFKLPKNSIT 527
QY 897 PLIMVPGTGVAPFRGFVQARKOLKEQOSGLBAHLYFGCRSPHEDYLYQEE--LENAQSE 955
Db 528 PVILIGTGTGAPLRGFRVRRVQOVKNVGNVGTLLFYGCRNSNEDFLYKQWAEYASVL 587
QY 956 G-LITLHTAFSRMPNPKTYVQHVMBQDGKLLLELDDOHAHFYICGDSQMAPAVEATLM 1014
Db 588 GENFEMFAPSRODPSKKVYVDKIENSOLVHELLTEGAIIVYCGDSARMARDVQTTIS 647
QY 1015 KSYADVHQVSEADARLWLOOLEEGRYAKDVW 1046
Db 648 KIVAKSREISEDKAAELVKSWKVQNYQEDVW 679

RESULT 15

US-10-138-905-83
; Sequence 83, Application US/10138905
; Publication No. US20030068800A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.

; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,905
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
; US-10-138-905-83

Query Match 10.9%; Score 597; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 2.1e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;
QY 430 ELDIKETLTKPEGFYVVKAKSKI-----PLGGIPSPSTEQSAKKVKKKAENAHNTPLLV 485
Db 5 KLDLYIITLVAVAAAFKQFLDQPDGTGFLNTDGSNSRDVLLTLKNNKNT--LLL 62
QY 486 YGSNMGTAEGTARDLADIAMSK--GFAPOVATLDH-----AGNLPREGAVLIVTASY-NGH 539
Db 63 FGSQTGAEDYANKLSRELHSRGLKTMVADFADYDWNFGDITDILVFFIVATYGE 122
QY 540 PPDNAKQFVDWLDQASADEVKGVYVSFGGDKNWTYQKVPF--IDETLAAGAEN 596
Db 123 PTNDAEFHTWLTE--BADTLSTLKYTVFGLGN-----STYEFFNAIGRKFDRLLSEKGGDR 177
QY 597 IADRGADASDDPEGTYEE-----WREHMWSDVAAYFNLD----- 631
Db 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234
QY 632 ---IENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQPGSARSTRHLEIEL 688
Db 235 DSQVSLGEPNKKYINSEGDILTKG--PFDHHT--PYLARITETRELFSS--SKDRHCHIVFE 291
QY 689 PK--EASYQEGDHLGVIPRNVGIVNRTARFGLDASQOIRLEAEE--EKLALHPLAKTVSV 746
Db 292 SESNLAYTTGDHLAIWPSNSDENIKQFAKFCGLEDKLDTVIELKALDSTYTFPPPIY 351
QY 747 EELLQ--YVELQDPVTRTQLRAMAAKTVCPPHKVLEALL-----EKQAYKEQVLAKRUTML 801
Db 352 GAVIRHLEITSGVPSRQFLSIAG---FAPDEETKKAFTRLGGDKQEFKAAKVTTRKFNIA 408
QY 802 ELL---EKPACEMKFESEFIALPSIRPRYYSISSSPRDEKQASITVSVSGEAWSGY 857
Db 409 DALLYSSNAPWSDVPEFLIENVPHLTPRYYSISS--SLSEKQLINVTAVVEAEADG 467
QY 858 GEYKGIASNYLAELQ-----EGDITTCFISPP-----OSEFTLPKDPET 896
Db 468 RPYTGVTNLLKNVEIVQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRNSNFKLPKNSIT 527
QY 897 PLIMVPGTGVAPFRGFVQARKOLKEQOSGLBAHLYFGCRSPHEDYLYQEE--LENAQSE 955
Db 528 PVILIGTGTGAPLRGFRVRRVQOVKNVGNVGTLLFYGCRNSNEDFLYKQWAEYASVL 587
QY 956 G-LITLHTAFSRMPNPKTYVQHVMBQDGKLLLELDDOHAHFYICGDSQMAPAVEATLM 1014
Db 588 GENFEMFAPSRODPSKKVYVDKIENSOLVHELLTEGAIIVYCGDSARMARDVQTTIS 647
QY 1015 KSYADVHQVSEADARLWLOOLEEGRYAKDVW 1046
Db 648 KIVAKSREISEDKAAELVKSWKVQNYQEDVW 679

Search completed: May 29, 2003, 08:27:08
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:12 ; Search time 163 Seconds
(without alignments)
4145.278 Million cell updates/sec

Title: US-10-031-146-2
Perfect score: 5457
Sequence: 1 TIKEMPOKTFGELKNPLLL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	5457	100.0	1048	24	US-10-031-695-2
4	5457	100.0	1049	1	PCT-US02-11954-2
5	5457	100.0	1049	21	US-09-791-537-53927
6	5457	100.0	1049	24	US-10-031-146-9

7	5457	100.0	1049	25	US-10-125-640-2
8	5457	100.0	1049	26	US-10-201-213-2
9	5449	99.9	1049	22	US-09-856-339A-21
10	5449	99.9	1049	24	US-10-018-730A-4
11	3314	60.7	1061	1	PCT-US02-11954-6
12	3314	60.7	1061	1	PCT-US02-11954-7
13	3314	60.7	1061	21	US-09-791-537-139768
14	3314	60.7	1061	25	US-10-125-640-6
15	3314	60.7	1061	25	US-10-125-640-7
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17	3281.5	60.1	1054	1	PCT-US02-11954-5
18	3281.5	60.1	1054	21	US-09-791-537-139586
19	3281.5	60.1	1054	25	US-10-125-640-4
20	3281.5	60.1	1054	25	US-10-125-640-5
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22	2461	45.1	471	21	US-09-791-537-71271
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24	2429	44.5	464	25	US-10-125-640-3
25	2429	44.0	458	21	US-09-791-537-116499
26	2386	43.7	455	21	US-09-791-537-8264
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28	1736.5	31.8	1066	21	US-09-791-537-139911
29	1736.5	31.8	1066	25	US-10-125-640-9
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31	1482.5	26.8	1115	25	US-10-125-640-10
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34	1002	18.4	191	21	US-09-791-537-116501
35	961	17.6	527	1	PCT-US02-11954-8
36	961	17.6	527	21	US-09-791-537-67053
37	961	17.6	527	25	US-10-125-640-8
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40	778.5	14.3	678	24	US-10-021-425-55
41	777.5	14.2	678	21	US-09-791-537-10974
42	777.5	14.2	678	24	US-10-021-425-54
43	777.5	14.2	686	21	US-09-791-537-12987
44	775.5	14.2	678	21	US-09-791-537-56962
45	775	14.2	678	21	US-09-791-537-118779

ALIGNMENTS

RESULT 1

US-10-031-146-2
; Sequence 2, Application US/10031146
; GENERAL INFORMATION:
; APPLICANT: HAUER, Bernhard
; APPLICANT: PLEISS, Juergen
; APPLICANT: SCHWANEBERG, Ulrich
; APPLICANT: SCHMITT, Jutta
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the ox
; TITLE OF INVENTION: organic substrates
; FILE REFERENCE: 50915
; CURRENT APPLICATION NUMBER: US/10/031.146
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect version 6.1
; SEQ ID NO 2
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-146-2

Query Match 100.0%; Score 5457; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TIKEMPOKTFGELKNPLLLNTDKPVQALMIADLGEIFKFEAPGRVTRVLSORLIKE 60
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Db 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSQRLIKE 60
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMKGYHAMV 120
Db 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMKGYHAMV 120
QY 121 DIAVOLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRNFNSFYRDOQPHPTITSMVRA 180
Db 121 DIAVOLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRNFNSFYRDOQPHPTITSMVRA 180
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIADRSKSGESDGLTLMHNG 240
Db 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIADRSKSGESDGLTLMHNG 240
QY 241 KDPETGEPLDENIRQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
Db 241 KDPETGEPLDENIRQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
QY 301 PVPYSYQVQKLVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360
Db 301 PVPYSYQVQKLVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360
QY 361 HRDKTWGDVVEEFRRPERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
Db 361 HRDKTWGDVVEEFRRPERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
QY 421 FDFEDHTNYELDIKETLTKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVKKAEHAHNT 480
Db 421 FDFEDHTNYELDIKETLTKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVKKAEHAHNT 480
QY 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
QY 541 PDNAKQFVWLDOASADEVKGVYRVSFVGCGDKKNWATYQKVPFIDETLAAGAENIADR 600
Db 541 PDNAKQFVWLDOASADEVKGVYRVSFVGCGDKKNWATYQKVPFIDETLAAGAENIADR 600
QY 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660
Db 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660
QY 661 AFSTNVVASKELQOQPGSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 720
Db 661 AFSTNVVASKELQOQPGSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 720
QY 721 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 721 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
QY 781 EALLERQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALLPISIRPRYYSISSSPRVDEK 840
Db 781 EALLERQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALLPISIRPRYYSISSSPRVDEK 840
QY 841 QASITVSVSGEAWSGYEGYKIASNYLAELQBGDITFCISTPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYEGYKIASNYLAELQBGDITFCISTPQSEFTLPKDPETPLIM 900
QY 901 VGPCTGVAPRGFVQARKOLKEQOQSLGEAHLFGCRSPHEDLYQOELENAQSEGIITL 960
Db 901 VGPCTGVAPRGFVQARKOLKEQOQSLGEAHLFGCRSPHEDLYQOELENAQSEGIITL 960
QY 961 HTAFSRMPNQPRTYVQVHVMQDQKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNQPRTYVQVHVMQDQKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADV 1020
QY 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048
Db 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048

; Sequence 35, Application US/10031241
; GENERAL INFORMATION:
; APPLICANT: Hauer, Bernhard
; APPLICANT: Schmid, Rolf D.
; APPLICANT: Schwaneberg, Ulrich
; TITLE OF INVENTION: Electron donor system for enzymes and its use in the biochemic
; TITLE OF INVENTION: conversion of substrates
; FILE REFERENCE: M/40076
; CURRENT APPLICATION NUMBER: US/10/031,241
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07251
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; US-10-031-241-35

Query Match 100.0%; Score 5457; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSQRLIKE 60
Db 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSQRLIKE 60
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMKGYHAMV 120
Db 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMKGYHAMV 120
QY 121 DIAVOLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRNFNSFYRDOQPHPTITSMVRA 180
Db 121 DIAVOLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRNFNSFYRDOQPHPTITSMVRA 180
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIADRSKSGESDGLTLMHNG 240
Db 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIADRSKSGESDGLTLMHNG 240
QY 241 KDPETGEPLDENIRQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
Db 241 KDPETGEPLDENIRQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
QY 301 PVPYSYQVQKLVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360
Db 301 PVPYSYQVQKLVGVNLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360
QY 361 HRDKTWGDVVEEFRRPERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
Db 361 HRDKTWGDVVEEFRRPERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420
QY 421 FDFEDHTNYELDIKETLTKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVKKAEHAHNT 480
Db 421 FDFEDHTNYELDIKETLTKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVKKAEHAHNT 480
QY 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
QY 541 PDNAKQFVWLDOASADEVKGVYRVSFVGCGDKKNWATYQKVPFIDETLAAGAENIADR 600
Db 541 PDNAKQFVWLDOASADEVKGVYRVSFVGCGDKKNWATYQKVPFIDETLAAGAENIADR 600
QY 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660
Db 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660
QY 661 AFSTNVVASKELQOQPGSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 720
Db 661 AFSTNVVASKELQOQPGSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRVTAARFGL 720
QY 721 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTOLRAMAAKTVCPPHKVEL 780


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Db 721 DASQIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
QY 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKSEFIALLPSPRYYISISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKSEFIALLPSPRYYISISSPRVDEK 840
QY 841 QASITVSVSGEAWSGYGKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
QY 901 VPGTGVAPRGFVQARKQLKEQCSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 901 VPGTGVAPRGFVQARKQLKEQCSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSOMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSOMAPAVEATLMKSYADV 1020
QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 3
US-10-031-695-2
; Sequence 2, Application US/10031695
; GENERAL INFORMATION:
; APPLICANT: Hauer, Bernhard
; APPLICANT: Pleiss, Jurgen
; APPLICANT: Schwaneberg, Ulrich
; APPLICANT: Schmitt, Jutta
; TITLE OF INVENTION: Modified cytochrome P450 monooxygenases
; FILE REFERENCE: M/40434
; CURRENT APPLICATION NUMBER: US/10/031.695
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07252
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-695-2

Query Match 100.0%; Score 5457; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIREMPOPKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 1 TIREMPOPKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
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Db 61 ACDESREDKLSQALKVRFVDFAGDGLFTSWTHEKNWKAHNNILLPSFSQAMKGYHAMV 120
QY 121 DIAVOLQVKERLNADSHIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQHPFTTSMVRA 180
Db 121 DIAVOLQVKERLNADSHIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQHPFTTSMVRA 180
QY 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240
Db 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240
QY 241 KDPETGEPDLDENTRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
Db 241 KDPETGEPDLDENTRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
QY 301 PVPSTKQVKQLKYGVGMVNLNEALRWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
Db 301 PVPSTKQVKQLKYGVGMVNLNEALRWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
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QY 361 HRDKTIWGDDVEEPRPERFENPNSAIPOHAFKPFNGORACIQCOQFALHEATLVLMMLKH 420
Db 361 HRDKTIWGDDVEEPRPERFENPNSAIPOHAFKPFNGORACIQCOQFALHEATLVLMMLKH 420
QY 421 FDFEDHTNYELDIKETITLTKPEGFVWAKSKKIPLGIPSPSTEQSAKKVRKKAENAHT 480
Db 421 FDFEDHTNYELDIKETITLTKPEGFVWAKSKKIPLGIPSPSTEQSAKKVRKKAENAHT 480
QY 481 PLLVLYCSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHGP 540
Db 481 PLLVLYCSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHGP 540
QY 541 PDNAKQFVMDLQASADEVKGVRYSVFQCGGDKNWTATYQKYPAFIDETLAAGKAENIADR 600
Db 541 PDNAKQFVMDLQASADEVKGVRYSVFQCGGDKNWTATYQKYPAFIDETLAAGKAENIADR 600
QY 601 GEADASDDPGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMFLAKMHG 660
Db 601 GEADASDDPGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMFLAKMHG 660
QY 661 AFSTNVVASKELQOPGSGARSTRHLEIELPKAEASQOEGDHLGVI PRNTEGIVNRVTAREGL 720
Db 661 AFSTNVVASKELQOPGSGARSTRHLEIELPKAEASQOEGDHLGVI PRNTEGIVNRVTAREGL 720
QY 721 DASQIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
Db 721 DASQIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
QY 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKSEFIALLPSPRYYISISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKSEFIALLPSPRYYISISSPRVDEK 840
QY 841 QASITVSVSGEAWSGYGKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
QY 901 VPGTGVAPRGFVQARKQLKEQCSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 901 VPGTGVAPRGFVQARKQLKEQCSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSOMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSOMAPAVEATLMKSYADV 1020
QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
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RESULT 4

PCT-US02-11954-2

; Sequence 2, Application PC/TUS0211954

; GENERAL INFORMATION:

; APPLICANT: Cirino, Patrick C.

; APPLICANT: Arnold, Frances H.

; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS

; FILE REFERENCE: 4058/2K237-WO0

; CURRENT APPLICATION NUMBER: PCT/US02/11954

; PRIOR FILING DATE: 2002-04-16

; PRIOR FILING DATE: 2001-04-16

; PRIOR FILING DATE: 2001-05-03

; PRIOR FILING DATE: 2001-12-12

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: Bacillus megaterium

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(1049)
PCT-US02-11954-2

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Query Match      100.0%; Score 5457; DB 1; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKLPNTDTPVQALMKIADELGEIFKFPAGRVTRYLSSQRLIKE 60
DB 2 TIKEMPOKTFGELKLPNTDTPVQALMKIADELGEIFKFPAGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 121
QY 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHPPITSMVRA 180
DB 122 DIAVQLVQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHPPITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQFEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240
DB 182 LDEAMNKLQANPDDPAYDENKRFQFEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEEAARVLD 300
DB 242 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEEAARVLD 301
QY 301 PVPYSYQVQKQLKYVGVNLEALRLWTPAFALSYAKEDTVLGGEYPLEKGDDELVLIPQL 360
DB 302 PVPYSYQVQKQLKYVGVNLEALRLWTPAFALSYAKEDTVLGGEYPLEKGDDELVLIPQL 361
QY 361 HRDKTWGDVVEEFRPERFENPSAIPQHAFFKPGNGQACIGQOQFALHEATLVLGMLKH 420
DB 362 HRDKTWGDVVEEFRPERFENPSAIPQHAFFKPGNGQACIGQOQFALHEATLVLGMLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLVGSNMGTAEGTARDLADTAMSKGFAPOVATLDSHAGNLPREGAVLIVTASNGHP 540
DB 482 PLLVLVGSNMGTAEGTARDLADTAMSKGFAPOVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLDOASADEVKGVYRYSVFGCGDKNWTATYQKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLDOASADEVKGVYRYSVFGCGDKNWTATYQKVPFIDETLAAKGAENIADR 601
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660
DB 602 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 661
QY 661 AFSTNVVASKELQOPGASRTHLELELPKEASYQEGDHLGVIPRNYEGIVNRTARFGL 720
DB 662 AFSTNVVASKELQOPGASRTHLELELPKEASYQEGDHLGVIPRNYEGIVNRTARFGL 721
QY 721 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAARTVCPPHKVEL 780
DB 722 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAARTVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTMELELKY PACEMKFSFIALPSPRIRYYSISSPRVDEK 840
DB 782 EALLEKQAYKEQVLAKRLTMELELKY PACEMKFSFIALPSPRIRYYSISSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGTASNYLAELQEGDTITCFSTPQSEFFLPKDPETPLIM 900
DB 842 QASITVSVSGEAWSGYGYKGTASNYLAELQEGDTITCFSTPQSEFFLPKDPETPLIM 901
QY 901 VPGTGVAPFRGVQARKQKQEGQSLGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 960
DB 902 VPGTGVAPFRGVQARKQKQEGQSLGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 961
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RESULT 5

US-09-791-537-53927

; Sequence 53927, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53927

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: Bacillus megaterium

; US-09-791-537-53927

Query Match 100.0%; Score 5457; DB 21; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 TIKEMPOKTFGELKLPNTDTPVQALMKIADELGEIFKFPAGRVTRYLSSQRLIKE 61
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QY 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEEAARVLD 300
DB 242 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEEAARVLD 301
QY 301 PVPYSYQVQKQLKYVGVNLEALRLWTPAFALSYAKEDTVLGGEYPLEKGDDELVLIPQL 360
DB 302 PVPYSYQVQKQLKYVGVNLEALRLWTPAFALSYAKEDTVLGGEYPLEKGDDELVLIPQL 361
QY 361 HRDKTWGDVVEEFRPERFENPSAIPQHAFFKPGNGQACIGQOQFALHEATLVLGMLKH 420
DB 362 HRDKTWGDVVEEFRPERFENPSAIPQHAFFKPGNGQACIGQOQFALHEATLVLGMLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLVGSNMGTAEGTARDLADTAMSKGFAPOVATLDSHAGNLPREGAVLIVTASNGHP 540
DB 482 PLLVLVGSNMGTAEGTARDLADTAMSKGFAPOVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLDOASADEVKGVYRYSVFGCGDKNWTATYQKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLDOASADEVKGVYRYSVFGCGDKNWTATYQKVPFIDETLAAKGAENIADR 601
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Qy 601 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661
Qy 661 AFSTNVVASKELOQPGSARSTRHLEIELPKEASVQEGDHLGVIPRNYEGIVNRTARFGL 720
Db 662 AFSTNVVASKELOQPGSARSTRHLEIELPKEASVQEGDHLGVIPRNYEGIVNRTARFGL 721
Qy 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
Qy 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSERIALLPSPRYYISISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSERIALLPSPRYYISISSPRVDEK 841
Qy 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901
Qy 901 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 961
Qy 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
Qy 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049
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RESULT 6

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US-10-031-146-9
; Sequence 9, Application US/10031146
; GENERAL INFORMATION:
; APPLICANT: HAUER, Bernhard
; APPLICANT: PLEISS, Juergen
; APPLICANT: SCHWANE, Ulf
; APPLICANT: SCHWITT, Jutta
; TITLE OF INVENTION: Novel cytochrome p450 monooxygenases and their use for the oxidat
; FILE REFERENCE: 50915
; CURRENT APPLICATION NUMBER: US/10/031,146
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect version 6.1
; SEQ ID NO 9
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-146-9
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Query Match 100.0%; Score 5457; DB 24; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TIKEMPQKTFGELKNLPILNTDKPVQALMKIADELGEIFKFPAPGRVTRVYLSQRLIKE 60
Db 2 TIKEMPQKTFGELKNLPILNTDKPVQALMKIADELGEIFKFPAPGRVTRVYLSQRLIKE 61
Qy 61 ACDESREDKNLSQALKVRDFAGDGLFTSWTHEKNKKKAHNILLPFSQOAMGYHAMV 120
Db 62 ACDESREDKNLSQALKVRDFAGDGLFTSWTHEKNKKKAHNILLPFSQOAMGYHAMV 121
Qy 121 DIAVOLQVQWERLNADIEHIEVPEDMTRLTDLTGLCGFNFRNSFYRQDPHPFTTSVRA 180
Db 122 DIAVOLQVQWERLNADIEHIEVPEDMTRLTDLTGLCGFNFRNSFYRQDPHPFTTSVRA 181
Qy 181 LDEAMNKLQRPANDDPAYDENKROFQEDIKVMNDLVKIIADRRKASGEQSDLLTHMLNG 240
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Db 182 LDEAMNKLQRPANDDPAYDENKROFQEDIKVMNDLVKIIADRRKASGEQSDLLTHMLNG 241
Qy 241 KDPETGPLEDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKQAEAAARVLVD 300
Db 242 KDPETGPLEDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKQAEAAARVLVD 301
Qy 301 PVPYSKYQVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDMLVLPQL 360
Db 302 PVPYSKYQVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDMLVLPQL 361
Qy 361 HRDKTIMGDDVEEERPERFENPSAIPQAHKPPGNGORACIGQGFALHEATLVLYGMLKH 420
Db 362 HRDKTIMGDDVEEERPERFENPSAIPQAHKPPGNGORACIGQGFALHEATLVLYGMLKH 421
Qy 421 FDEEDHNYELDKETLTLPKEGVVKAISKIPLGIPSPSTQSKAKYKKAENAHNT 480
Db 422 FDEEDHNYELDKETLTLPKEGVVKAISKIPLGIPSPSTQSKAKYKKAENAHNT 481
Qy 481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 541
Qy 541 PDNAKQFVMDLQASADEVKGVRYSVFCGCKGNWATTYQKVPAFIDETLAAGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRYSVFCGCKGNWATTYQKVPAFIDETLAAGAENIADR 601
Qy 601 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661
Qy 661 AFSTNVVASKELOQPGSARSTRHLEIELPKEASVQEGDHLGVIPRNYEGIVNRTARFGL 720
Db 662 AFSTNVVASKELOQPGSARSTRHLEIELPKEASVQEGDHLGVIPRNYEGIVNRTARFGL 721
Qy 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
Qy 781 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSERIALLPSPRYYISISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELEKYPACEMKFSERIALLPSPRYYISISSPRVDEK 841
Qy 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901
Qy 901 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFYGCRSPHEDYLYQEELENAQSEGIITL 961
Qy 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
Qy 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049
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RESULT 7

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US-10-125-640-2
; Sequence 2, Application US/10125640
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/1K237-US3
; CURRENT APPLICATION NUMBER: US/10/125,640
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
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;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 60/340,602
;; PRIOR FILING DATE: 2001-12-12
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 2
;; LENGTH: 1049
;; TYPE: PRT
;; ORGANISM: Bacillus megaterium
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: GenBank / P14779
;; DATABASE ENTRY DATE: 1990-04-01
;; RELEVANT RESIDUES: (1)..(1049)
US-10-125-640-2

Query Match 100.0%; Score 5457; DB 25; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE 60
DB 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVOLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYRNSFYRDPHPFITSMVRA 180
DB 122 DIAVOLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQARNPDDPAYDENKROFQEDIKVMNDLVDKIIADKASGESQDILLTHMLNG 240
DB 182 LDEAMNKLQARNPDDPAYDENKROFQEDIKVMNDLVDKIIADKASGESQDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLD 301
QY 301 PVPSTKQVKQLKYGWNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELWLIPOL 360
DB 302 PVPSTKQVKQLKYGWNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELWLIPOL 361
QY 361 HRDKTIWDDVEEFRPERFENPSAIPQHAFKPFNGQACIGIQQFALHEATLVGLMMLKH 420
DB 362 HRDKTIWDDVEEFRPERFENPSAIPQHAFKPFNGQACIGIQQFALHEATLVGLMMLKH 421
QY 421 FDFEDHTNLDIKETLTILKPGFVVKAKSKKIPIGGIPSPSTEQSAKKVKKAEHAHNT 480
DB 422 FDFEDHTNLDIKETLTILKPGFVVKAKSKKIPIGGIPSPSTEQSAKKVKKAEHAHNT 481
QY 481 PLLVLGYNMGTAEGTARDLADIAKSGFAPQVATLDHAGNLPREGAVLIYVTSYNGHP 540
DB 482 PLLVLGYNMGTAEGTARDLADIAKSGFAPQVATLDHAGNLPREGAVLIYVTSYNGHP 541
QY 541 PNAKQFVWLQOASADEKGVYRVYVFGCGDKNWTATYOKVPFADITETLAAGAENIADR 600
DB 542 PNAKQFVWLQOASADEKGVYRVYVFGCGDKNWTATYOKVPFADITETLAAGAENIADR 601
QY 601 GEADASDDFEGTYEERHWSDAVAFNLDIENSEDNKSTLSLOFVDSAADMPKMHG 660
DB 602 GEADASDDFEGTYEERHWSDAVAFNLDIENSEDNKSTLSLOFVDSAADMPKMHG 661
QY 661 AFSTNVVASKELQPGSARSTRHLEIELEPKEASYQEGDHLGVIIPRYEGIVNRVYARFGL 720
DB 662 AFSTNVVASKELQPGSARSTRHLEIELEPKEASYQEGDHLGVIIPRYEGIVNRVYARFGL 721
QY 721 DASQIIRLEAEBEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPKPKVEL 780
DB 722 DASQIIRLEAEBEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPKPKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFFIALPSIRPRYVSISSSPRVDEK 840
|||||

DB 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFFIALPSIRPRYVSISSSPRVDEK 841
QY 841 QASITVSVVSGEAWSGYGYKGIASNYLAELOEGDITICFISTPOSEFTLPKDPETPLIM 900
DB 842 QASITVSVVSGEAWSGYGYKGIASNYLAELOEGDITICFISTPOSEFTLPKDPETPLIM 901
QY 901 VGPGTGVAPFRGFGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYOELENAQSEGIITL 960
DB 902 VGPGTGVAPFRGFGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYOELENAQSEGIITL 961
QY 961 HTAFSRMPNQPKTYVQHVMEQDGKLIELLDGHAHYICDGSQMAPAVEATLMKSYADV 1020
DB 962 HTAFSRMPNQPKTYVQHVMEQDGKLIELLDGHAHYICDGSQMAPAVEATLMKSYADV 1021
QY 1021 HGVSEADARLWLQOLEEKGRYAKDYWAG 1048
DB 1022 HGVSEADARLWLQOLEEKGRYAKDYWAG 1049

RESULT 8

US-10-201-213-2
; Sequence 2: Application US/10201213
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; APPLICANT: Farinas, Edgardo
; APPLICANT: Glieder, Anton
; APPLICANT: Arnold, Frances
; APPLICANT: Schwanberg, Ulrich
; TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES
; FILE REFERENCE: 3369/1K238-US2
; CURRENT APPLICATION NUMBER: US/10/201,213
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 60/306,766
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/308,429
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(1049)
US-10-201-213-2

Query Match 100.0%; Score 5457; DB 26; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE 60
DB 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVOLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYRNSFYRDPHPFITSMVRA 180
DB 122 DIAVOLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQARNPDDPAYDENKROFQEDIKVMNDLVDKIIADKASGESQDILLTHMLNG 240
DB 182 LDEAMNKLQARNPDDPAYDENKROFQEDIKVMNDLVDKIIADKASGESQDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLD 301
QY 301 PVPSTKQVKQLKYGWNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELWLIPOL 360

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Db 302 PVPYKQVQLKLVGMVNEALRLWPTAPAFSLYAKEDTVLGGEVPLEKGDLMVLIPQL 361
QY 361 HRDRTINGDDVEEERPERFENPSAIPQHAFFPGNGQACIGQGFALHEATLVIGMLKH 420
Db 362 HRDRTINGDDVEEERPERFENPSAIPQHAFFPGNGQACIGQGFALHEATLVIGMLKH 421
QY 421 FDFEDHNYELDIKETLTLPKEGFVVKAKSKKIPGGIPSPSTQSAKKVKKKAENAHNT 480
Db 422 FDFEDHNYELDIKETLTLPKEGFVVKAKSKKIPGGIPSPSTQSAKKVKKKAENAHNT 481
QY 481 PLLVLYSGNMGTAEGTARDLADIAWSKGAFQVATLDHAGNLPREGAVLIVTASNGHP 540
Db 482 PLLVLYSGNMGTAEGTARDLADIAWSKGAFQVATLDHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYKQPAFTDETAAKGAENATDR 600
Db 542 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYKQPAFTDETAAKGAENATDR 601
QY 601 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 660
Db 602 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 661
QY 661 AFSTNVVASKELQPGSARSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQPGSARSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKSEFIALPLPSIRPRYSISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKSEFIALPLPSIRPRYSISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFITSTQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFITSTQSEFTLPKDPETPLIM 901
QY 901 VPGTGVAPFRGFGVQARKQKQSGSLEAHLYFCGRSPHEDYLYQEELENAQSEGIITL 960
Db 902 HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1021
QY 1021 HOVSEADARLWLOQLEKGRYAKDVWAG 1048
Db 1022 HOVSEADARLWLOQLEKGRYAKDVWAG 1049
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RESULT 9

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US-09-856-339A-21
; Sequence 21, Application US/09856339A
; GENERAL INFORMATION:
; APPLICANT: Wong, Luet
; APPLICANT: Bell, Stephen
; APPLICANT: Carmichael, Angus
; TITLE OF INVENTION: PROCESS FOR OXIDISING TERPENES
; FILE REFERENCE: HO-P021960S0 (10104571)
; CURRENT APPLICATION NUMBER: US/09/856.339A
; CURRENT FILING DATE: 2001-05-18
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: GB 9825421.2
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
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; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1049)
; OTHER INFORMATION: Coding sequence
US-09-856-339A-21

Query Match 99.9%; Score 5449; DB 22; Length 1049;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPOKPTGELKNLPDLLNTDPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKPTGELKNLPDLLNTDPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 61
QY 61 ACDSERFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSPFSQAKMGVHAMV 120
Db 62 ACDSERFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSPFSQAKMGVHAMV 121
QY 121 DIAVOLVQKWERLNADHEIEVPEDMTRTLTDTIGLCGFNYRFSYRQDPHPFITSMVRA 180
Db 122 DIAVOLVQKWERLNADHEIEVPEDMTRTLTDTIGLCGFNYRFSYRQDPHPFITSMVRA 181
QY 181 LDEAMNKLQANPDPPAYDENKRFQEDIKYANDLVDKIIADRKASGQSDLLTHMLNG 240
Db 182 LDEAMNKLQANPDPPAYDENKRFQEDIKYANDLVDKIIADRKASGQSDLLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 300
Db 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 301
QY 301 PVPYKQVQLKLVGMVNEALRLWPTAPAFSLYAKEDTVLGGEVPLEKGDLMVLIPQL 360
Db 302 PVPYKQVQLKLVGMVNEALRLWPTAPAFSLYAKEDTVLGGEVPLEKGDLMVLIPQL 361
QY 361 HRDRTINGDDVEEERPERFENPSAIPQHAFFPGNGQACIGQGFALHEATLVIGMLKH 420
Db 362 HRDRTINGDDVEEERPERFENPSAIPQHAFFPGNGQACIGQGFALHEATLVIGMLKH 421
QY 421 FDFEDHNYELDIKETLTLPKEGFVVKAKSKKIPGGIPSPSTQSAKKVKKKAENAHNT 480
Db 422 FDFEDHNYELDIKETLTLPKEGFVVKAKSKKIPGGIPSPSTQSAKKVKKKAENAHNT 481
QY 481 PLLVLYSGNMGTAEGTARDLADIAWSKGAFQVATLDHAGNLPREGAVLIVTASNGHP 540
Db 482 PLLVLYSGNMGTAEGTARDLADIAWSKGAFQVATLDHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYKQPAFTDETAAKGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYKQPAFTDETAAKGAENIADR 601
QY 601 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 660
Db 602 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 661
QY 661 AFSTNVVASKELQPGSARSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQPGSARSTRHLEIELPKESYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKSEFIALPLPSIRPRYSISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKSEFIALPLPSIRPRYSISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFITSTQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFITSTQSEFTLPKDPETPLIM 901
QY 901 VPGTGVAPFRGFGVQARKQKQSGSLEAHLYFCGRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VPGTGVAPFRGFGVQARKQKQSGSLEAHLYFCGRSPHEDYLYQEELENAQSEGIITL 961
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QY 961 HTAFSRMPNPKTYVHVMEQDGKLIETLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVHVMEQDGKLIETLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049
RESULT 10
US-10-018-730A-4
; Sequence 4, Application US/10018730A
; GENERAL INFORMATION:
; APPLICANT: Luet, Wong
; APPLICANT: Jonathan, Jones
; TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
; FILE REFERENCE: P02353051 / 10112404 / N.76277B
; CURRENT APPLICATION NUMBER: US/10/018,730A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: GB 9914373.7
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/GB00/02379
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-018-730A-4

Query Match 99.9%; Score 5449; DB 24; Length 1049;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPOPTFGELKMLPLINTDKPVQALMKIADELGEIFKFPAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOPTFGELKMLPLINTDKPVQALMKIADELGEIFKFPAPGRVTRYLSSORLIKE 61
QY 61 ACDESFRDKNLQALFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 120
Db 62 ACDESFRDKNLQALFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 121
QY 121 DIAVOLQVQRWLNADHEIEVPEDETRLTLDITGLGCFNYRNFNSFYRDOHPHPIITSMVRA 180
Db 122 DIAVOLQVQRWLNADHEIEVPEDETRLTLDITGLGCFNYRNFNSFYRDOHPHPIITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMDLVDKIADRKASGEQSDLLTHMLNG 240
Db 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVMDLVDKIADRKASGEQSDLLTHMLNG 241
QY 241 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 300
Db 242 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD 301
QY 301 PVPYSQVQKQKYVGMVNLALRLWTPAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 360
Db 302 PVPYSQVQKQKYVGMVNLALRLWTPAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO 361
QY 361 HRDKTWDDVEFRERENPNSAIPQHAFAKPPGNGQRACIGQOQFALHEATLVGLMMLKH 420
Db 362 HRDKTWDDVEFRERENPNSAIPQHAFAKPPGNGQRACIGQOQFALHEATLVGLMMLKH 421
QY 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIPSPTEQSAKKVKAENAHNT 480
Db 422 FDFEDHTNYELDIKETLTKPEGFVVKAKSKKIPLGIPSPTEQSAKKVKAENAHNT 481
QY 481 PLLVLXGNSMGTAEGTARDLADLAMSKEGAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 482 PLLVLXGNSMGTAEGTARDLADLAMSKEGAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKFVWDLQASADEVKGVYRVSFVCGCGDKNWTYQKVPAPAFIDETLAAGAENIADR 600

Db 542 PDNAKFVWDLQASADEVKGVYRVSFVCGCGDKNWTYQKVPAPAFIDETLAAGAENIADR 601
QY 601 GEADASDDFEGYEEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660
Db 602 GEADASDDFEGYEEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661
QY 661 AFSTNVVASKELQOQPGSARSSTRHLEIETLPEKASQYQGDHLGVIPRNVYEGIVNRTARFGL 720
Db 662 AFSTNVVASKELQOQPGSARSSTRHLEIETLPEKASQYQGDHLGVIPRNVYEGIVNRTARFGL 721
QY 721 DASQQIRLEAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 722 DASQQIRLEAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPISIRYYSISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPISIRYYSISSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPGTGVADPFRGVQARKOLKEQOQSLGEAHLFYGCRSPHEDYLYOELENAQSEGIITL 960
Db 902 VGPGTGVADPFRGVQARKOLKEQOQSLGEAHLFYGCRSPHEDYLYOELENAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVHVMEQDGKLIETLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVHVMEQDGKLIETLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 11

PCT-US02-11954-6
; Sequence 6, Application PC/TUS0211954
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-WOO
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / 008394
; DATABASE ENTRY DATE: 2001-10-16
; RELEVANT RESIDUES: (1)..(1061)
PCT-US02-11954-6

Query Match 60.7%; Score 3314; DB 1; Length 1061;
Best Local Similarity 59.5%; Pred. No. 1e-287;
Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;
QY 5 MPQKTFGELKMLPLINTDKPVQALMKIADELGEIFKFPAPGRVTRYLSSORLIKEACDE 64
Db 7 IQPQTFGELKMLPLINTDKPVQALMKIADELGEIFKFPAPGRVTRYLSSORLIKEACDE 66
QY 65 SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMVADI 124

67	Db	EREDK5LEGALEKVRAPSGDGLTSWHTEPNWKAHNILMPTFSQAMKDHYHEKMVDIAV	136
125	QY	QLVQKWERLNADHEIIVPEDMTRLTDTIGLCGFNTFNSFYRQDPHPTFTSMVRALDEA	184
127	Db	QLIOKWARLNPNEADVPGDMTRLTDTIGLCGFNTFNSYRETPHPTFNSMVRALDEA	186
185	QY	MNKLQANPDPPAYDENKQFQBDIKVMNDLVDKIADRAKASEQSD--DLTTIMLNGKDP	243
187	Db	MQHQRLDVODKLMWRTKKQFRYDQITMFSLVDSIIAERRANGDQDEKDLARLMLNVEDP	246
244	QY	ETCEPLDDENIRYQIITFIAGHETTSGLLSFALYFLVKNPVHLQRAAEAAARVLVDVPP	303
247	Db	ETCEKLDENIRFOIITFIAGHETTSGLLSFPATYFLKKHPDKLKKAYEEVDVTDAAAP	306
304	QY	SYKQVKQLKVVGMVLNEALRLWPTAPAFSLYAKEDVTVLGGEYPLEGDELMVLIPQLHRD	363
307	Db	TYKQVLELTYIRMLNESLRLWPTAPAFSLYKEDVTIGVKKFTITNDRISVLIPQLHRD	366
364	QY	KTTWGDDVEEPFEREFENPSAIPOHAFKPGNGQACIGOOFAHLEATVLGHMLKHDF	423
367	Db	RDAGWKADEEFEREHEQDQVPHHAYKPGNGQACIGMPAFHLEATVLGHMLKYFTL	426
424	QY	EDHNTYELDTIKETLTLKPGFVVYKAKSKKIPLGGIPSPSTEQA---KKYRKAENA---	477
427	Db	IDHENTYELDTIKQVTLTKPGDFHISVQSRHQEATHADVQAAKAAPEQKEKTEAGASVI	486
478	QY	--HNTPLVLVYGSNMGTAGCTARDLAIAMSKGFAQVATLDSHAGNLPEGAVLIVTAS	535
487	Db	GLNNRPLVLVYGSDTGTAEGVARELADTASLHGVRTKPTAPLNDRIKLPKEGAVIVTSS	546
536	QY	YNGHPDPNAKQFYDWLDDQASADVGVYKSVFCGDKNWAITYQKVPFAFIDETLAARGAE	595
547	Db	YNGKPPSNAGQFYQWLQEIKPGELEGVHYAVFCGDBHNWASTYQYVREFIDEQAEKGAT	606
596	QY	NIADRGFADASDDFEGTYEWRHMSDVAAYFNLDI--ENSEDNKSTLSLQFVDSAADMP	654
607	Db	RFARGEQGVSGDFEGOLDKWKSMADATKAFGLELNEADKERSTLSLQFVRGLGESP	666
655	QY	LAKWHGAFSTNVYASKELOQPGSARSTRHLEIELPKEASYOEGDHLGVIPRNTYEGIVNRV	714
667	Db	LARSYEASHASIAENRELOSADSDRSTRHTEIALPPDVEYQEGDHLGVLPKNSQTNVRSI	726
715	QY	TARFGLDASQOIRLEAAEEKLAHLPLAKTVSVBELIQQ--VELQDPTVRTQIRAMAQTVVC	773
727	Db	LHRFGLKGTQDVTLSAGRSAGHLPLGRPVSLHDLLSYSEVQEPAAIRAQIRELASFTVC	786
774	QY	PPHKVELEALLERQAYKEQVLAKRLTLMLELLEYKACEMKFSFETLPIRPRYKSISS	833
787	Db	PPHRELEELSAGVYQEQBQILKKRISMLDILEXYEACDMPFERFLELLRPLKPRYKSISS	846
834	QY	SPRVDEKQASITVSVYSGEAWSGYKGTASNYLAEQLQBDGTITCFISTPQSEFTLPKD	893
847	Db	SPRVNPRQASITVGVVRPAWSGRGEYRGVASNDLAERQAGDDVYMFIRTPESRQLPKD	906
894	QY	PETPLIMVGPCTGVAPRGFVQARKOLKEQOGSILGEAHLFYGCGRSPHEDLYLQOELENAQ	953
907	Db	PETPLIMVGPCTGVAPRGFGLQARDVLKREGKTLGEAHLFYGCGRN--DRDFTYRDELERFE	965
954	QY	SEGIITLHTAFSRMPNQPTQYOVHVBQDKKILTELIDQGAHFYICGDGSGMAPAVETLL	1013
966	Db	KDGIIVTHTAFSRKEGNPKTYVQHLMADQADTLLSIDRGRGLYVCGDGSKMAPDVEAAL	1025
1014	QY	MKSYADVHQVSEADARLWLOOLEEKGRIYAKDVWAG	1048
1026	Db	QKAYQAVHGHTGEQEAQNLWHLHODTQMGYAKDVWAG	1060

```

; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-WO0
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / D69799
; DATABASE ENTRY DATE: 2000-07-28
; RELEVANT RESIDUES: (1)..(1061)
; PCT-US02-11954-7

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Query Match	60.7%	Score 3314;	DB 1;	Length 1061;
Best Local Similarity	59.5%;	Pred. No. 1e-287;		
Matches 628;	Conservative 156;	Mismatches 259;	Indels 12;	Gaps 6;
QY	5	MPQKTFGELKNIPLLNTDQPVQALMKIADLGEIFKFEAPGRVTRVLSORLIKEACDE	64	
DB	7	IPQKTFGPGNLPLLDKDXPTLSLKLAEOQPIFOIHTPAGTIVVSGHELKVEYCD	66	
QY	65	SREDKNLSQALKFVRDFAGDGLTSTWTHKKNKAHNILPSPSSQQAQKGYHAMMDIAY	124	
DB	67	ERDPKSTEGALEKVRAPSGDGLFTSWTHPNWKAHNILMPTFSQRAKMDYHEKQVDIAY	126	
QY	125	QLYQKKERLNADSHIEVPEDMTRLTLDITGLCGFNRYFNSFYRDOPHPFTTSMVRALDEA	184	
DB	127	QLQKKARLNPNPAVDVPGDMTRLTLDITGLCGFNRYFNSFYRTPHPFTFNSVWRALDEA	186	
QY	185	MNKLORANPDPAIDENKROFQEDIKVMNDLVPKIIADRKASGQSD-DLLTHMLNGKDP	243	
DB	187	MHQQRLDVQDKLMVTRTKQFRYDIQPMFSLVDSIIAERRANGDQDEKDLARMLNVEDP	246	
QY	244	ETGEPDDEINRYOILTFETLAGHETTSGLLSFALYFLVKPNPHVLQKAAEARVLDPVP	303	
DB	247	ETGEKLDDEINRFQILITFLTAGHETTSGLLSFAYFLFKHPDKLUKAYEEDRVLTDAAP	306	
QY	304	SYKQVKQLKYGVMVLNLEALRLWTPAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOLHRD	363	
DB	307	TYKQVLELYIRMLNESLRLWTPAPAFSLYPREDTVIGCKFPITTNDRISVLIPQLHRD	366	
QY	364	KTTWGDVDFEERFERFENPSAIPQAHKPKPGNGQACIGQOFALHEATVLVGMMLKHDFD	423	
DB	367	RDANGKDAEEFRPERFEHQDQPHHAYKPKPGNGQACIGMQFALHEATVLVGMMLKFTL	426	
QY	424	EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGISPSTEOSA---KKYKKKAENA---	477	
DB	427	IDHENTYELDIKQITLTKPGGFHISVQSRHQEAIHADYQAAEKAPDDQCKEATEANGASVI	486	
QY	478	--HNTPLLVLYSGNMGTAEGTARDLADIAISKGFAPQVATLDSHAGMLPREGAVLIYVTS	535	
DB	487	GLNNRPLLVLYSGDGTAEGVARELADTASLHGVRTKTAPLNDRIGKLPREGAVVIYVTS	546	
QY	536	YNGHPDPAKQFVDWLDAQSADEVKGVVRYSVFEGCGDKNWTATYQKVPAFIDETLAAGAE	595	
DB	547	YNGKPPSNACQFQWQLQEIKPGEJGELVHYAVFVCGGDHNNWASTYQYVPRFIDEQLAEGAT	606	
QY	596	NIADRGADASDDFEGYEWREHMHWSDVAAFYNLDI-ENSEDNKSTLSLQFVDSADMP	654	
DB	607	RFSGRGGDVSQDFEGQLDCEKWSMWADATKAPGLNELNNAKDERSTLSQFYVKGLESP	666	
QY	655	LARKMHGAFSTNVYASKELQOPGASRSTRHLEIELPKAESYQEGDHLGVIPRNYEGIVNR	714	

; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank / O08394
 ; DATABASE ENTRY DATE: 2001-10-16
 ; RELEVANT RESIDUES: (1)..(1061)
 US-10-125-640-6

Qy	5	MPQKTFGELKNPLNLTDPVQALMKIADLGEIFKFEAPGRVTRYSORLIKEACDE	64
Db	7	IPQKTFGLNGLNPLIDKDKPTLSLIKLAEEQGFQIHTPAGTIVVSGHELKVCDE	66
Qy	65	SRFDKNSLQALKFVRDAGDGLFTSWTHKNNKKAHNLPSFSQOAKMGVHAMVVDIAV	124
Db	67	ERFDKSTEGALEKVRASGDLFTSWTHKNNKKAHNLMPFSQOAKMGVHAMVVDIAV	126
Qy	125	QVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYFNPSYRDPQPHFTSMVRALDEA	184
Db	127	QVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYFNPSYRDPQPHFTSMVRALDEA	186
Qy	185	MNKLQANPDPPAYDENKRFQEDIKVMNDLVKIIADKASGEQSD-DLLTHMLNGKOP	243
Db	187	MNKLQANPDPPAYDENKRFQEDIKVMNDLVKIIADKASGEQSD-DLLTHMLNGKOP	246
Qy	244	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	303
Db	247	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	306
Qy	304	SYKOVKOLKYVGMVNLNEALRWPTAPASLYAKEDTVLGGEYPLEKGDLMVLIPQLHRD	363
Db	307	TYKOVLELTYRMLNLSLRLWPTAPASLYAKEDTVLGGEYPLEKGDLMVLIPQLHRD	366
Qy	364	KTINGDVEEPRPERFENPSAIPQAHKPFNGORACIGQOQFALHEATLVGLMKLHFD	423
Db	367	RDANGKDAEPRPERFENPSAIPQAHKPFNGORACIGQOQFALHEATLVGLMKLHFD	426
Qy	424	EDHTNYELDKETITLTPKPGFVVRKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	477
Db	427	IDHENYELDKETITLTPKPGFVVRKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	486
Qy	478	--HNTPLLVLYGSMGTAGTARDLADTAMSKGPAQOVATLDSHAGNLPRGAVLIYVTS	535
Db	487	GLNRRLLVLYGSDTGAEGVARELADTASLHGVRTKTAPLNDRIGLKPKEGAVVIVTS	546
Qy	536	YNGHPPDNKQFVMDLQASADEVKGVRYSVEGCGDNWATYQVPAFIDETLAAGAE	595
Db	547	YNGHPPDNKQFVMDLQASADEVKGVRYSVEGCGDNWATYQVPAFIDETLAAGAE	606
Qy	596	NIADRGADSDDEGTYEEMRHHWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP	654
Db	607	RFSGRGDVSDFEGQLDEWKKSWADAIAKAFGLNELNADKERSLQFVGLGESP	666
Qy	655	LAKMHGAFSTNVASKELQOPGARSARSTRHLEIPLKEASQOEGDHLGVIPRYEGIVNR	714
Db	667	LARSYEASHASIAENRELQSDSRSTRHIEALPPDVEYQEGDHLGVLPKNSQTNVSRI	726
Qy	715	TAREGLDASQIRLEAEEKLAHLPLAKTVSVELLOY-VELQDPVTRTQLRAMAAKTV	773
Db	727	LHREGLKGTQDVTLSASGRSAGHLPLGRPSVLHLLSYSVQVAAATRAQIRELASTVC	786
Qy	774	PPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALPSIRPRYSISS	833
Db	787	PPHRELELSAEGVQEQILKKISMILLLEKYEACDMPFERLELLRLPKPRYSISS	846
Qy	834	SPRVDEKQASTVSVSGEAMSGYGEYKGIASNYLAELQEGDITCTISTPQSEFTLPKD	893
Db	847	SPRVNPROASTVGVGRGPAWSGRGEYRGVANSNDLAERQAGDDVVMVTRTPESRFQPKD	906
Qy	894	PETPLIMVPGTGVAPRGFVQARKOLKEQOQSGLGEAHLPGCRSPHEDYLYQELENAQ	953
Db	907	PETPLIMVPGTGVAPRGFVQARKOLKEQOQSGLGEAHLPGCRN-DRDFTYRDELENER	965

; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank / O08394
 ; DATABASE ENTRY DATE: 2001-10-16
 ; RELEVANT RESIDUES: (1)..(1061)
 US-10-125-640-6

Qy	954	SEGIITLHTAFSRMPNPKTYVQVHMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATL	1013
Db	966	KDGIIVTHTAFSRKEGPKTYVQVHMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATL	1025
Qy	1014	MKSYADYHVOVSEADARLWLQOLEEKRYAKDVWAG	1048
Db	1026	KQAYQAVHGTGEQEAQNWRLHLDQTMGYAKDVWAG	1060

RESULT 15
 US-10-125-640-7
 ; Sequence 7, Application US/10125640
 ; GENERAL INFORMATION:
 ; APPLICANT: Cirino, Patrick C.
 ; APPLICANT: Arnold, Frances H.
 ; TITLE OF INVENTION: PROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
 ; FILE REFERENCE: 4058/1K237-US3
 ; CURRENT APPLICATION NUMBER: US/10/125,640
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/284,215
 ; PRIOR FILING DATE: 2001-04-16
 ; PRIOR APPLICATION NUMBER: 60/288,636
 ; PRIOR FILING DATE: 2001-05-03
 ; PRIOR APPLICATION NUMBER: 60/340,602
 ; PRIOR FILING DATE: 2001-12-12
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 1061
 ; TYPE: PRT
 ; ORGANISM: Bacillus subtilis
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank / D69799
 ; DATABASE ENTRY DATE: 2000-07-28
 ; RELEVANT RESIDUES: (1)..(1061)
 US-10-125-640-7

Qy	5	MPQKTFGELKNPLNLTDPVQALMKIADLGEIFKFEAPGRVTRYSORLIKEACDE	64
Db	7	IPQKTFGLNGLNPLIDKDKPTLSLIKLAEEQGFQIHTPAGTIVVSGHELKVCDE	66
Qy	65	SRFDKNSLQALKFVRDAGDGLFTSWTHKNNKKAHNLPSFSQOAKMGVHAMVVDIAV	124
Db	67	ERFDKSTEGALEKVRASGDLFTSWTHKNNKKAHNLMPFSQOAKMGVHAMVVDIAV	126
Qy	125	QVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYFNPSYRDPQPHFTSMVRALDEA	184
Db	127	QVOKWERNLNADEHIEVPEDMTLTDITGLCGFNRYFNPSYRDPQPHFTSMVRALDEA	186
Qy	185	MNKLQANPDPPAYDENKRFQEDIKVMNDLVKIIADKASGEQSD-DLLTHMLNGKOP	243
Db	187	MNKLQANPDPPAYDENKRFQEDIKVMNDLVKIIADKASGEQSD-DLLTHMLNGKOP	246
Qy	244	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	303
Db	247	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	306
Qy	304	SYKOVKOLKYVGMVNLNEALRWPTAPASLYAKEDTVLGGEYPLEKGDLMVLIPQLHRD	363
Db	307	TYKOVLELTYRMLNLSLRLWPTAPASLYAKEDTVLGGEYPLEKGDLMVLIPQLHRD	366
Qy	364	KTINGDVEEPRPERFENPSAIPQAHKPFNGORACIGQOQFALHEATLVGLMKLHFD	423
Db	367	RDANGKDAEPRPERFENPSAIPQAHKPFNGORACIGQOQFALHEATLVGLMKLHFD	426
Qy	424	EDHTNYELDKETITLTPKPGFVVRKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	477
Db	427	IDHENYELDKETITLTPKPGFVVRKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	486

Result No.	Score	Match	Length	DB	ID	Description
1	2420.5	44.4	1077	6	US-10-214-446-24	Sequence 24, Appl
2	1945.5	35.7	1073	6	US-10-156-761-8117	Sequence 8117, Ap
3	953.5	17.5	504	6	US-10-156-761-14954	Sequence 14954, A
4	777.5	14.2	677	6	US-10-219-051B-11638	Sequence 11638, A
5	777.5	14.2	677	6	US-10-219-051B-12755	Sequence 12755, A
6	769.14	14.1	682	6	US-10-148-907A-23	Sequence 23, Appl
7	767.14	14.1	676	6	US-10-219-051B-12757	Sequence 12757, A
8	767.14	14.1	677	7	US-60-440-068-572	Sequence 572, App
9	728.5	13.3	689	6	US-10-424-599-187294	Sequence 187294, A
10	712.5	13.1	719	6	US-10-425-114-70174	Sequence 70174, A
11	710.5	13.0	691	6	US-10-424-599-191313	Sequence 191313, A
12	705.5	12.9	588	6	US-10-188-523B-14	Sequence 14, Appl
13	705.5	12.9	588	6	US-10-188-523C-14	Sequence 14, Appl
14	688	12.6	708	6	US-10-424-599-177338	Sequence 177338, A
15	678	12.4	1429	5	US-09-661-258-2	Sequence 2, Appl
16	675	12.4	1199	7	US-60-452-680-23982	Sequence 23982, A
17	675	12.4	1199	7	US-60-453-135-14960	Sequence 14960, A
18	675	12.4	1199	7	US-60-453-050-14960	Sequence 14960, A
19	675	12.4	1199	7	US-60-453-444-8116	Sequence 8116, Ap
20	675	12.4	1199	7	US-60-465-241-8116	Sequence 8116, Ap
21	675	12.4	1434	5	US-09-661-258-1	Sequence 1, Appl
22	665.5	12.2	1144	5	US-09-751-708A-124	Sequence 124, App
23	665.5	12.2	1144	5	US-09-661-258-5	Sequence 5, Appl
24	665	12.2	1153	5	US-09-661-258-4	Sequence 4, Appl
25	661	12.1	1114	5	US-09-724-676-86297	Sequence 86297, A
26	661	12.1	1114	5	US-09-724-676A-86297	Sequence 86297, A

Db 245 TGVDRTTGEOLDVNNIRYQINTELIAGHETTSGLLSCTLYALLKHPHLLRKYAEYEDRVL 304
QY 299 ---VDPVPSYQVQKQYKQVGMVNEALRLWPTAPAFSLYAKEDTVLGGVEYPLEKGDLMW 355
Db 305 GPDINARPYQVQYTOITQILKEALRLWPPAPAYGIGPLKDETIGGKYKLLKNFTIV 364
QY 356 LIPOLHRDKTIGDDVEEPRPERF--ENPSAIPQHAFFKPGNGQRACIGQOQFALHEATLV 413
Db 365 LVLLALHRDSVMSGNDPAEDPENSREAEARFINAWKPGNGQRACIGRFAMHEAALA 424
QY 414 LGMMLKHEFEDHTNYELDIKELTKLPGFVVK----AKSKIPILGGTIPS-----PSTEQ 465
Db 425 IGMILREFKLVVNNRYOMWLKFTLTKPDGFKIKYRPAERDRGAYGGAASVAMAGNTPT 484
QY 466 SAKKVRKKAENAHNTPLLVYSGNMGTAEGTARDLADIAKMSKFAPOVATLDSHAGNLP 525
Db 485 AP---HERPLGHTPLLVYSGNLTGAELATRVADLAEVNGFATKLAPLDDFVGKLEP 541
QY 526 EGAVLIVTASYNHPPDNKAKQFVDWL--DOASADEVGVRYSVFGCGDKNWTATYQVPAP 584
Db 542 QGVLIFCASYNGVPPDNATQFVKWLGDDIPKDSFAKRYAVYFGCGNSDWAATYQSVPL 601
QY 585 IDETLAAGAENTADGEADASDDFEGTYEWEHMSDVAAYFNLD--IENSEDNKSTL 642
Db 602 IDEQLAAGARSYTTREGDARSLDGQFESWFPAFAAATAATREFLESNFSRSDAPLY 661
QY 643 SLQFVDSAADMPLAKMHGAFSTVNVASKELQBP---GSAKSRHLEIELPLKEASYQEGD 698
Db 662 TIEPVAPSVVNTIVTQGGVLPKRVVANSLOKNGTNPDSRSTRHVEVQLPPGISYRVD 721
QY 699 HLGVIPTNTEGVNRYTARGLDASQOIRLEAEKEELAHPLAKTVSVBELL--QYVELQD 757
Db 722 HLSVVRNDPALVDVARRFGLPADQIRLQVAEGRRALPVGDAVSGRLLTFEVELQ 781
QY 758 PVTRTOLRAAAKTCPPHKEVLEALEKQA-----YKEQVLAKRLTMLELEKYPACEM 812
Db 782 VATRKQIILSEHTRCPMTKPLKVLGAGDDASAERYRAELGVKRSVFDLLEHFACE 841
QY 813 KFEFIALPSIRPRYISSSSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYLAELQ 872
Db 842 PPHAFLEMLSLAPRYISSSSPAGEPARCSVTAAVASPASSGRGIYRGVCSNYLAGRR 901
QY 873 EGTITCFISTPOSETFLPKDPTPLIMVPGTGVAPFRGVQARQLKEQOGLGEHL 932
Db 902 AGDTIHATVRETKAGFLRPNDSVPITIMIGPGTGLAPFRGFLQERAAQAAGATLGPAML 961
QY 933 YFCRSPHEDYLOELENQAQSGIITLHTAFRMPNQPKTYVOHYMEODGKKLIELLQ 992
Db 962 FFCRHPEDQYLYADELKAFAADGITEHTAFSR--GDGPKTYVOHLIVAEKRVCSLIEQ 1020
QY 993 GAHYICGDSQMAPAEATLMKSYADVHQVSEADARLWLQOLEEKRYAKDVWAG 1048
Db 1021 GAIIVYCGDGRMEPDVKATLVGIYRERSGADAGTAQRWIEDLGAKNRYVLDVWAG 1076

RESULT 2

US-10-156-761-8117
; Sequence 8117, Application us/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8117
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-8117

Query Match 35.7%; Score 1945.5; DB 6; Length 1073;
Best Local Similarity 38.2%; Pred. No. 2.4e-160;
Matches 417; Conservative 195; Mismatches 408; Indels 71; Gaps 17;

QY 7 QPKT-----FGEKLNPLLLNTDKPVQALMKIADELGE-IFKFEAPGRVRYL 52
Db 4 QPETHLRPIRSRPGVPLFGHTPQIPSTN---PVEYFGKLSKQPEGLGMEIAGIQVEFV 60
QY 53 SQORLIKEACDSRFPDKNLSQA-LKFVRDFAGDGLTSTWHEKNWKAHNILLPSFQA 111
Db 61 WPDVLVAEYCDRETFKQIDKTPLAHVRYAGAGLFTAHOHEEWGMAHRVLLPVFSQA 120
QY 112 MKGYHAMVYDIAVLQVQKWERLNADSHIEVPEDMTRLTLDITGLCGFNRYNSFYRDQPH 171
Db 121 MKGYFCQMLEIAQNLVQKWER--KEGPVNITDDYTRLTDTALSFGYRFDSEFAKEDLH 179
QY 172 PFTTSMVRALDEA-----MNKLQANPDDPAYDENKROFQEDIKVNLDLVKLIAD 222
Db 180 PFLNALLQALVESLRSSQELPVMTKMRKA--DDKKYREN-----IRLMDLVENVIKE 230
QY 223 RK-ASGEQSDLLTHMLNGKDPETGEPLDDENTIRYIITFLIAGHETTSGLLSFLYFLV 281
Db 231 RREGKGTGEDDLGLGLEATDPETGKGLDDNDVQVTVFLIAGHETTSGLLSFATYSLM 290
QY 282 KNPVHLQKAAEAARVLV--DPVPSYQVQKQVGMVNEALRLWPTAPAFSLYAXZEDTV 340
Db 291 RNPHILLAAAYAEVDRLLPDGTVPDYDTIMQMDVIPRLSETLRLWAPIWIGKSPLEDTV 350
QY 341 LGGEVPLEKGDLMVLIPOLHRDKTITWDDVEEPRPERFENFSAIPQ-----HAPKPF 393
Db 351 IGGCYGLKKGARVNILEGLPHTHPKAW-----RPEEFDINRLPENRVNHHPHAYKPF 404
QY 394 GNGORACIGQAFALHEATLVLMKLFHDFEDHTNYELDIKELTKLPGFVVKAKSKKI 453
Db 405 GNGVRACIQRFALTEARLALALVLOKFKFADDDTYKMDVKEALTRKPGGFELNVRQAE 464
QY 454 PLGGIPSPSTEQSAKVRKKAENAHNTPLLVYSGNMGTAEGTARDLADIAKMSKFAPOV 513
Db 465 HERTVGAADIQTDDTQAQAAVSGVGVNLTVAYSGSLGSCEDLARTIADRGERSGFGTTL 524
QY 514 ATLDSHAGNLPREGAVLIVTASYNHPPDNKAKQFVDWLQOASAD-EVKGVRYSVFGCGDK 572
Db 525 VGLDELGDNLPTGELLVVVYASSYNGKAPDNAQRFDLLAAGLPEGSLSNVRFALLAGANT 584
QY 573 NNATYQKVPATFDETLLAAKGAENTADGEADASDDFEGTYEWEHMSDVAAYFNLDI 632
Db 585 QWATYQGGPKRIEAGLLAAGATRVIERGIADAAGDFDGMATRWMDTLMTLAEETAAAD- 643
QY 633 ENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTVNVASKELQBP-----RSTR 682
Db 644 -TSETTGPREFVQLLTAEEVRPAIVSEQAYPLTVVANEELVSDATGLWDFSTIEPPRAAK 702
QY 683 HLEIELPKESYQEGDHLGVIPRNTYEGIVNRYTAREGLDASQOIRLEAEKEELAHPLAK 742
Db 703 SITIELPDGVTYDTGNHLAVFAKNEPVLNRLARLGVDRDQVLRDQPGGGRTHLPVGT 762
QY 743 TVSVLELL-QYVELQDPVTRTOLRAAAKTCPPHKEVLEALL-----EKOAYKEOVLA 796
Db 763 PVTGGLLTFEVELQDVATRSQIQELAEHTQCPTWRPQLQAYTADTAEBERYKQKILK 822
QY 797 RLTMLELEKYPACEMKFSEFIALPSIRPRYISSSSPRVDEKQASITVSVSGEAWSG 856
Db 823 RYSVNLNLEREPAVELPLAVFLEMGPPIRPREYISSSSPLANRHRVRLTVGLLEGFALSG 882
QY 857 YGEYKGIASNYLAELQEGDTITCFISTPOSETFLPKDPTPLIMVPGTGVAPFRGVQ 916

QY 934 FCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQKTYVQHVMEQDGKGLIELLDQ 992
Db YGCRSDEYLYREELARFKDGLQNLVAFSR-EQAHKVVYVQHVLLKRDREHLWKLIHE 621
QY 993 -GAHFYICGDSGOMAPAVEATLMKSYADYVHQVSEADARLWLOOLEKGRYAKDVA 1047
Db 622 GGAHIYVCGDARNMAKDQVNTFYDVAEFGPMEHTQAVDYVKKLMTKGRYSLDWS 677

RESULT 5

US-10-219-051B-12755
; Sequence 12755, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 12755
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41064
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-12755

Query Match 14.2%; Score 777.5; DB 6; Length 677;
Best Local Similarity 32.2%; Pred. No. 1.6e-58;
Matches 211; Conservative 111; Mismatches 263; Indels 71; Gaps 23;

QY 444 FVVKAKSKKIP---LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLVYSGNMGTAEGTAR 498
Db 41 FFRKKKEIPESKIQTTAPPVKSESSFVERMKKTGRN-----IIVFGSQGTAEAFAN 95
QY 499 DLADIAMSGFAPOVATLDH---AGNLP--EGAVLIVTASY-NGHPDPAKQFVDWL 551
Db 96 RLKSDAHRGMRGMSADPEYDLADLSLPEIDKSLVFCMATYGEGETDQNAQFYDWL 155
QY 552 DQASADEVKGVYSGCGDKNWTYQKVA---FIDETLAAKAENIADRGADASD 608
Db 156 QETDVD-LGVKFAVFLGNK---TYEHFNAMGVYDQRLQGLAQRIFELGLGDDGN 210
QY 609 FEGTYEWEHWMDSVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMH----- 659
Db 211 LEEDFITWREQFWPACVCEFFGVEATGESSIRQYELVHE---DMDVAKVYTGEMGRKLS 267
QY 660 -----GAFSTNVVASKELQOPGARSRTHLIEL-PKEASYQEGDHLGVIPRY 707
Db 268 YENQKPPDPAKPNFLAAVTANRKLQ-GTERHLMHLELSDSKIRYESGDHVVYPAND 326
QY 708 EGIVNRVTARFG--LDASQIILEAEKEKLAHLPLAKTVSVBELQYVLEQDPVTRTQLR 765
Db 327 SALVNIQIGILGADLDVIMSLNLDSESNKKHPPCPTTYRTALTAYLDTNP-PRTNVL 385
QY 766 AMAAKTVCP-----HKVELEALLEKQAYKEQVLAKRLTLMLELEKYPACEMKSEFTA 819
Db 386 YELAQVASEPSQEHLLHKMASSGEGEKLYLSWVVEARRHILAILQDYPSPRLPDIHCE 445
QY 820 LLPSPRPRYSISSPRVDEKQASITVSVSGEAMSGYGEYGIASNYL-AELQEGDT-- 876
Db 446 LLPRLQARYSIASSKVPHPNSVHICAVAVEYEAKSGRVN-KGVATSWLRAKEPAGENG 504
QY 877 ---ITCFISTPOSETTLPKDPTPLIMVGPFGTVAPFRGTVQARKQLKEQGOSLGEAHL 933

Db 505 RALVPMFVR--KSQFLRPFKSTTPVIMVGPFGTGIAPFMGFIQERAWLRQEGVEGETLLY 562
QY 934 FCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQKTYVQHVMEQDGKGLIELLDQ 992
Db YGCRSDEYLYREELARFKDGLQNLVAFSR-EQAHKVVYVQHVLLKRDREHLWKLIHE 621
QY 993 -GAHFYICGDSGOMAPAVEATLMKSYADYVHQVSEADARLWLOOLEKGRYAKDVA 1047
Db 622 GGAHIYVCGDARNMAKDQVNTFYDVAEFGPMEHTQAVDYVKKLMTKGRYSLDWS 677

RESULT 6

US-10-148-907A-23
; Sequence 23, Application US/10148907A
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Compositions and Methods for Hologenation Reactions
; FILE REFERENCE: S-31082A
; CURRENT APPLICATION NUMBER: US/10/148,907A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/228801
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/219343
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-148-907A-23

Query Match 14.1%; Score 769; DB 6; Length 682;

Best Local Similarity 31.7%; Pred. No. 9e-58;
Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;

QY 444 FVVKAKSKKIP---LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLVYSGNMGTAEGTAR 497
Db 45 FFRKKKEIPESKIQTTAPPVKSESSFVERMKKTGRN-----IIVFGSQGTAEAFAN 99
QY 498 DLADIAMSGFAPOVATLDH---AGNLPREGAVLIV--TASY-NGHPDPAKQFVDW 550
Db 100 NRLSDAHRGMRGMAADPEYDLADLSLPEINNALAVFCMATYGEGETDQNAQFYDW 159
QY 551 LQASADEVKGVYSGCGDKNWTYQKVA---FIDETLAAKAENIADRGADASD 607
Db 160 QETDVD-LGVKFAVFLGNK---TYEHFNAMGVYDQRLQGLAQRIFELGMGDDA 214
QY 608 FEGTYEWEHWMDSVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMH----- 659
Db 215 NLEEDFITWREQFWPACVCEFFGVEATGESSIRQYELVL---HTDIDVAKVYQEGMRUK 271
QY 660 -----GAFSTNVVASKELQOPGARSRTHLIEL-PKEASYQEGDHLGVIPRN 706
Db 272 SYENQKPPDPAKPNFLAAVTANRKLQ-GTERHLMHLELSDSKIRYESGDHVVYPAN 330
QY 707 YGIVNRVTARFGLDASQOI---RLEAEKEKLAHLPL-----AKTVSV 746
Db 331 DSALVNIQIGILGADLDVIMSLNLDSESNKKHPPCPTTYRTALTAYLDTNPRTNVL 390
QY 747 EELQYVLEQDPVTRTQLRAMAATVCPHPKVELEALLEKQAYKEQVLAKRLTLMLELEK 806
Db 391 YELAQVA--ADPAEQELRKMASSG-----EGKELYLSWVVEARRHILAILQD 437
QY 807 YPACEMKSEFTALLPSRPRYSISSPRVDEKQASITVSVSGEAMSGYGEYGIASNY 866
Db 438 YPSLRPPDHLCELLPRLQARYSIASSKVPHPNSVHICAVAVEYETKAGRLN-KGVATS 496
QY 867 YL-AELQEGDT-----ITCFISTPOSETTLPKDPTPLIMVGPFGTVAPFRGTVQARKOL 920
Db 497 WLRKEPAGENGGRALVPMFVR--KSQFLRPFKSTTPVIMVGPFGTGIAPFMGFIQERAWL 554

Db 509 VPMFVR--RSQRLPFKATTPVIMVPGTGVAPFICGIERAWLRQOGKEVGETLLYYGC 566
QY 937 RSPHEDYLOEELNASEGIIIT-LHTAFSRPNQPTVVOHVMEQDGKKLELLDQGAH 995
Db 567 RRSDEYLYREELAQPHRGALQTNVAFSRQSH-KYVVOHLKQDRHLWKLIEGGAH 625
QY 996 FYICGDSQMAPAVEATLMKSYADHVQVSEADARLWLOOLEKRGYAKDVWA 1047
Db 626 IYVCGDARNMARDVQNTFYDIYVAELGAMHAQAVDIKKLMTYKGRYSLDWS 677

RESULT 9

US-10-424-599-187294
; Sequence 187294, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187294
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(689)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140138C.1.pep
US-10-424-599-187294

Query Match 13.3%; Score 728.5; DB 6; Length 689;
Best Local Similarity 31.2%; Pred. No. 3.2e-54;
Matches 195; Conservative 102; Mismatches 256; Indels 73; Gaps 20;
QY 480 TPLLVLVGNMGTAETARDLAD--IAMSKGAPQVATLDSHA-----GNLPREGAVL 530
Db 78 TRVAIFGQTGTAEAGFAKALAEIEIKARYEKAQVADLDYADDDQYEEKLKESLAF 137
QY 531 IVTASY-NGHPDPNAQOFVDWLDQASADEVKGV-----RYSVFGCGDKNWATTYQKVPF 584
Db 138 FMLATYGDGEPTDAAAFYKWTTEGK-DE-RGIWLXQLYGVGFLGNROY-EHFNKIGKI 194
QY 585 IDETLAAGAENIADRGADADSDDFEGTYEEWRHMSDVAAYFNLDIENSEDNKSTLSL 644
Db 195 VDEELSEQAKRLVPLGLGDDQSIEDDFVANKESLWSELD-----QLLRDEDDVNTVST 249
QY 645 QF-----VDSADMPL-----AKMHGAFSTNNVASKELQPGSART 581
Db 250 PYKAAIPEYRVVTHDSTVTSNDNHLNVANGNAVFDIHPCRVNTIAAARELHKPESDRSC 309
QY 682 RHEIELPKEA-SYQEGDHLGVIPRYNIGVNRVTARFGLDASQQLRLEAEELKLAHPL 740
Db 310 IHLEFDISGTGIYFEGDHVGVFAENGDEVEAGKLLQODLDLVSFIHTNED--GTP 367
QY 741 AKTVSVVE-----ELQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KOA. 788
Db 368 GSSLPPFPFGPCTLRFAAHYADLLNPPRKASIVALAANTSEPPSEADRLTFLSSPOGKDE 427
QY 789 YKEQVLAKRLTMLELEKYPACEMKSEFI-ALLPSIRPRYYSISSPRVDEKQASITVS 847
Db 428 YSKWLVSQSLLEVNAAEPFSAKPPILGVFFAAVAPHQLQPRYYSISSPRFSQKVHTCA 487
QY 848 VSGEAWSGYGEYKGIASNYLAEL-----LAEIQEDTITCFISTPQSEFTLPKDPETPLIMV 901
Db 488 LVCGPTPTG-RIHKGVCSTWMNAIPLEKSRDCSWAPIFVR---SNFKLPADHSTPLIMV 544

QY 902 GPGTGVAPRGRFVQAKQKLEQOQSLGEARHLYFGCRSPHEDYLOEELNASEGIIIT-L 960
Db 545 GFGTGLAPRGRFLOERLALKEDAVQLGPAALLFGCNRQMDFIYEDELANEMEQALSSEL 604
QY 961 HPAFSRMPNQPRTYVQHVMEQDGKKLELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 605 IVTFSR-EGPEKEYVQHKMKDKAANLWNLISQGGYLVCGDAKGMDVHRTLHRTIVQOQ 663
QY 1021 HOVSEADARLWLOOLEKRGYAKDVW 1046
Db 664 ENVDSKAEAIYKVKLQMDGRYLRLDVM 689

RESULT 10

US-10-425-114-70174
; Sequence 70174, Application US/10425114
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70174
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73168A03_FLI.pep
US-10-425-114-70174

Query Match 13.1%; Score 712.5; DB 6; Length 719;
Best Local Similarity 30.1%; Pred. No. 8.8e-53;
Matches 188; Conservative 109; Mismatches 250; Indels 78; Gaps 21;
QY 484 VLYGSMGTAGTATADLADIAMSK--GFAPQVATLDSHA-----GNLPREGAVLIVTA 534
Db 111 IFPGTGTGTAEAGFAKSAEAEARAYEKAVFVVDLDYAAQEDDEYEELKKTETVFLFLA 170
QY 535 SY-NGHPDPNAQOFVDWLDQASADEV--KGVYRVFGCGDKNWATTYQKVPFIDFTLAA 591
Db 171 TYGDGEPTDAAAFYKWTTEGKEKEVWLKDLKYGIFGLGNROY-EHFNKAVKVDLVEE 229
QY 592 KGAENIADRGADADSDDFEGTYEEWRHMSDVAAYFNLD--IENSED-----637
Db 230 QGGKRLVPVGLGDDQCIEDDFATMKELWPE-----LDQLLRDEDDFTGASTPYTAAL 283
QY 638 -----NKSTLSLQFVDSADMDPLAKMHGAFS-----TNVASKELQPGSARSTRH 583
Db 284 PEYRVVFDKSLDSFQ-----DRSWTLANGTVIDIQHPCRSVAVRKEHLKPAASRSCI 339
QY 684 LHEIELPKEA-SYQEGDHLGVIPRYNIGVNRVTARFGLDASQQLRLEAEEL-----733
Db 340 LEFDISGTGLVYETGDHGVYAENSQVTVVEVERLLDLPDFFSHADAEDGSPKGGG 399
QY 734 KLAHLPLAKTVSVE-ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAY 789
Db 400 SLAP-PFSPSPCTLRALTALRYADLLNPPKKAALLALASHASDPAEAEERFLASPSKDEY 458
QY 790 KEOVLAKRLTMLELEKYPACEMKSEFI-ALLPSIRPRYYSISSPRVDEKQASITVS 848
Db 459 SQMITASQSLLEVNAAEPFSAKPPILGVFFAAVAPHQLQPRYYSISSPRKMAPSRHVTAL 518
QY 849 VSGEAWSGYGEYKGIASNYLAEL-----LAEIQEDTITCFISTPQSEFTLPKDPETPLIMV 902
Db 519 VYGPPTG-RIHKGVCSTWMNAIPLEKSRDCSWAPIFVR---QSNFKLPADHSTPLIMIG 575

Db 477 GCRNRKVDYFIYENLNFFVENCALSELDMASFR-EGASKEYVQHKMSQKASDIWNMLSEG 535
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHQSVEADARLWLOOLEEGRYAKDVW 1046
Db 536 AYLVCGDAGKMAKDVHRTLHTIVQEQNLDSKAEIYKYNLQNSGRYLDDW 588

RESULT 13

US-10-188-523C-14
; Sequence 14, Application US/10188523C

; GENERAL INFORMATION:

; APPLICANT: Tang, Xiao-Song

; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID

; FILE REFERENCE: BC1009-CIP

; CURRENT APPLICATION NUMBER: US/10/188,523C

; CURRENT FILING DATE: 2002-10-24

; PRIOR APPLICATION NUMBER: US 09/627,216

; PRIOR FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: US 60/147,719

; PRIOR FILING DATE: 1999-08-06

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: MICROSOFT OFFICE 97

; SEQ ID NO 14

; LENGTH: 588

; TYPE: PRT

; ORGANISM: Helianthus tuberosus

US-10-188-523C-14

Query Match 12.9%; Score 705.5; DB 6; Length 588;
Best Local Similarity 31.9%; Pred. No. 2.5e-52;
Matches 189; Conservative 92; Mismatches 245; Indels 67; Gaps 19;

QY 499 DLADLAMSKEGPAQVATLDSHAGNLPREGAVLIVTASY-NGHPDPAKQFVDWLQASAD 557
Db 18 DLDVY-----ADDEEVAEKKETFAFFFLATVGDGEPTDAAAFYKWFTEG--- 65
QY 558 EVKGV-----RYSVEGCGDKNWTYQKVPFIDETLAAGAENIADREASDDFEGT 612
Db 66 DDKGVLEKHLHYGVFGVGLGNKQY-EHFNKIALVVDGLTEOGAKRFPVPGVGLGDDQSI 124
QY 613 YEEWEHMKSDVAAYFNLDIENSNDKS-----TSLSL-----QFVDSADNPL 655
Db 125 FSAMEKLWPELDQLL-ID-----EDDKTAATPYTAAIPEYRVVFDHDKPDTFSENHSQ 179
QY 656 AKMHGA-----FSTNVVASKELQPGSARSTRHLEIPLKREA-SYQGDHLGVIPRYEGIV 711
Db 180 HTVHDAQHPCRSNVAVKELHTPESDRSCTHLEFDISHGTSYETGDHGVYCNLEIVV 239
QY 712 NRVTFARFGLDASQQLRLAEAEKLAHL-----PLAKTVSVEELLQVVELQDPVTRTOL 764
Db 240 EEAERLGLPADTYFSLHIDNEDGTPGGPTLQPPFPCTLRKALTNYADLLSSPKKSTL 299
QY 765 RAMAAKTVCPPHKHVELEALLE---KQAYKEQVLAKRLTMELEKYPACEMKFSEFI-AL 820
Db 300 LALAHASDATEADRLQFLASREGKDETAEMVANSRLLEVMAEFSAKPLPVFFFAAI 359
QY 821 LPSIRPRYISISSPRVDEKQASITVSVSSEANSYGEYKGIASNY-----LAELOEG 874
Db 360 APRLOPRYISISSPKMVPNRHVTALVY-EKTPGGRIHKGICSTWKNVAVPLTENQDC 418
QY 875 DTITCFISTPOSEFTLPKDPETPLIMVGGTGVAFPGFVQARKOLKQGGSLGAHLYF 934
Db 419 SSAPIFVTR--SNRFLPADPKVPVIMIGPGTGLAPFRGLORLAKESGELGQSILFF 476
QY 935 GCRSPHEDYLYQEELENAQSGEII--LHTAFSRPNQPKTYVQHVWEDQKLELLDQ 993
Db 477 GCRNRKVDYFIYENLNFFVENCALSELDMASFR-EGASKEYVQHKMSQKASDIWNMLSEG 535
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHQSVEADARLWLOOLEEGRYAKDVW 1046
Db 536 AYLVCGDAGKMAKDVHRTLHTIVQEQNLDSKAEIYKYNLQNSGRYLDDW 588

RESULT 14

US-10-424-599-177338

; Sequence 177338, Application US/10424599

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 177338

; LENGTH: 708

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(708)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_131152C.1.pcp

US-10-424-599-177338

Query Match 12.6%; Score 688; DB 6; Length 708;

Best Local Similarity 28.7%; Pred. No. 1.2e-50;
Matches 190; Conservative 114; Mismatches 269; Indels 90; Gaps 21;

QY 447 KAKSKKIP---LGGTSPSPSQSAKKVRKKAENAHNTPLLVLYGSMGTAGTARDLADI 503
Db 73 KAKPLEPPKRVVKKLPELEIVDDGKVV-----TILFGTQGTGAEFAKATAEE 120
QY 504 AMSK--GFAPOVATLDSHAGN-----LPREGAVLIVTASY-NGHPDPAKQFVDWLQ 553
Db 121 AKARYEKATFRVDDMDYAADDDDEYERFKKETHVLFVFLATYGDGEPTDAAAFYKWFTE 180
QY 554 ASADE---VKGVRKSVFCGCKNWTYQKVPFIDETLAAGAENIADREASDDF 610
Db 181 GGEKGEGLWQLHGVFGVGLGNKQY-EHFNKVAKVVDMLVEQGGKRLVPVGLGDDQDCIE 239
QY 611 GTYEEWEHMKSDVAAYFNLDIENSNDKSTLSLQFVDSA-----ADMPLAKM 658
Db 240 DDFATWKEELWP-----ALDELLRDEDDATVSTPYTAAVLEYRVVIHDPLEASVDEK 293
QY 659 HGA-----FSTNVVASKELQPGSARSTRHLEIPL-KEASQEGDHLGVIPRN 706
Db 294 HNVNGHAIYDQHPVRANVAVRKELHTPADRSCTHLEFDISHGTSYETGDHGVYCN 353
QY 707 YEGIVNRVTFARFGLDASQQLRLAEAE-----KLAHL-----LAKTVSVEELLQVVEL 755
Db 354 LSEVVEEAIIRLIGLSPDTYFISIHTDDEGKPRSGSLPPTFPCTLRFA-----LARYADV 409
QY 756 QDPVTRTOLRAMAAKTVCPPHKHVELEALLE---KQAYKEQVLAKRLTMELEKYPACE 811
Db 410 LSSPKKSALLAALAHASDPSSEADRLHXLXASAPAGKDEYSEWVIAQSORSLLVMAEFPSAK 469
QY 812 MKFSEFT-ALLPSTRPRYISISSPRVDEKQASITVSVSSEANSYGEYKGIASNY--- 867
Db 470 PPIGVFFAAVAPRLQPRFYISISSPRMVPNRHVTALVHVKEMPTG-RIHGVCSTWKN 528
QY 868 ---LAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGGTGVAFPGFVQARKOLKEOG 924
Db 529 SVPLEKSDCQSWAPIFVTR--SNRFLPSDNKVPVIMIGPGTGLAPFRGLORLAKKEGG 586
QY 925 QSLGAHLYFCRSPHEDYLYQEELENAQSGEII--LHTAFSRPNQPKTYVQHVWEDQ 983
Db 587 AELGPSVLFFCRRNQMDYIYDELSHFVNTGALDELILAFSR-EGPTKEYVQHKMMEKA 645
QY 984 KKLLELLDQGAHFYICGDSQMAPAVEATLMKSYADVHQSVEADARLWLOOLEEGRYAK 1043

QY	1023	VSEADARLWLQQLLEKGRYAKDVW	1046
		: : : : : :	
Db	1372	LSEEDAGVFISRLRDDNRYHEDIF	1395

Search completed: May 29, 2003, 08:26:31
Job time : 58 secs

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RESULT 15
US-09-661-258-2
; Sequence 2, Application US/09661258
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-661-258-2

```

Query Match	12.4%	Score	678;	DB	5;	Length	1429;
Best Local Similarity	28.2%	Pred.	No. 3.4e-49;				
Matches	193;	Conservative	126;	Mismatches	265;	Indels	100;
Gaps	20;						
QY	457	GIFSPSTEQSAKKVRKAE	-----NAHNTPLLYVSGNMGCTAGETARDIADIA	504			
Db	718	GTNGTPTKRAIGFKKLAENAVKS	AKLMGQAMAKRVKATILYATETGSKOAYAKTLCEIF	777			
QY	505	MSKGFAPOAVTDLSHAGNLPGRE	GAIVLTASY--NGHPDPAKOF-----	547			
Db	778	KHAFDAKAMSEEDYDVHLEHEAL	YLVVTFGNGDPDENGKEFGCALMEMRHPNSVQEE	837			
QY	548	-----	-----VMDLQ--ASADEVKGVRYSVFEGCGDKNNAWATTYQKVP	582			
Db	838	RKSKYKVRFNSVSSYSDRSKSG	DPDLDRNFESTGPLANRVFSVFGLSR-----AYPHFC	893			
QY	583	AF---IDETLAAKGAENIADRG	EADSDDEFCYIEEWRHWSDDVAAYFNL--DIENSED	637			
Db	894	AFGHAVDTLLEELGGERILKMR	EGDELCGOEEAFRTWAKKVFKAACDVFVCGDDVNTKEP	953			
QY	638	NKSTLS-----	LOFVDSAADMP--LAKWH--GAFSTNVVASKELQPGCSARSTR	682			
Db	954	NNSLISNDRSWKRNKPF	LTVVAEAPDUTQGLSNVHKHKAARLSQNLQSPKFSRSTI	1013			
QY	683	HLEIEL--PKEASYQEGDH	LGVPTRNYEGIVNRVTARF--GLDASQOIRLEAEKELAHL	738			
Db	1014	FVRLHTNGNQLQYQPGDHLG	VFPNGHEDLVNALIERLEDAPPANHVVVKVEMLEERTAL	1073			
QY	739	PLAKTVSVEELL-----	QYVELODPVTRTQTLRAMAAKTVCPPHKVELEALLE-KQ	787			
Db	1074	GVISNWKDESRLPPCTIFQ	AKFYLDITPTPTLQLOQFASLATNEKEKORLLVLSGLQ	1133			
QY	788	AYKEOVLAKLTLMLELLEK	PACEMKFSFIALLPSIRPRYSITSSSPRVDKQASTVVS	847			
Db	1134	EYEWKGGKPTWVEVLEEPS	LOMPATLLLTLSLQPPRYSITSSSPDMPYDVBVHTVA	1193			
QY	848	VVSGEAWSGYGE-YKGIASNY	LAELQEGDITTCFISTPQSEFTLPKDEPTPLMGVPGTG	906			
Db	1194	IVSYHTRDGEGPVHHGVCS	WNLNRIQADVVVPCFVRGAPS-FHLPRNPVPCILVGGCTG	1252			
QY	907	VAPFRGVQARK-OLKEQGS	QLGSAHLYFCGRSPHEDYLYQOELENAQSEGIIL-TLHTAF	964			
Db	1253	IAPERSFWQORQEDIOHKG	MNCPMWLVFGCRQSKIDHIVREETLOAKNKGVFRELYTAY	1312			
QY	965	SRMPNQPKTYVQHVMEODG	KKLI--ELLDOGAHFYICGDSQMAPAVETILMKSYADVHQ	1022			
Db	1313	SREPRPKKYQDVLOQSAE	SVYRALKEGGHIVYCGDVTMAADVLKA-IQRLTMOQGG	1371			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:26:36 ; Search time 49 seconds
(without alignments)
2056.099 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKEMPQKTFGELKNPL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5457	100.0	1049	1 A34286	NADPH-ferrithemopro
2	3314	60.7	1061	2 D69799	cytochrome P450 /
3	3281.5	60.1	1054	1 A69975	NADPH-ferrithemopro
4	777.5	14.2	678	1 RDR704	NADPH-ferrithemopro
5	769	14.1	677	1 RDP004	NADPH-ferrithemopro
6	767	14.1	679	2 A25505	NADPH-ferrithemopro
7	767	14.1	677	2 A60557	NADPH-ferrithemopro
8	761.5	14.0	678	2 S27158	NADPH-ferrithemopro
9	739.5	13.6	692	2 T05582	NADPH-ferrithemopro
10	737.5	13.5	681	2 T14903	NADPH-ferrithemopro
11	735.5	13.5	671	2 A56592	NADPH-ferrithemopro
12	723	13.2	601	2 A28577	NADPH-ferrithemopro
13	723	13.2	690	2 A47298	NADPH-ferrithemopro
14	711.5	13.0	683	2 T10720	NADPH-ferrithemopro
15	711	13.0	692	2 S37159	NADPH-ferrithemopro
16	709	13.0	711	2 T14081	NADPH-ferrithemopro
17	706	12.9	705	2 T10723	NADPH-ferrithemopro
18	705.5	12.9	590	2 S37157	NADPH-ferrithemopro
19	705	12.9	699	2 T14904	NADPH-ferrithemopro
20	702.5	12.9	712	2 S21531	NADPH-ferrithemopro
21	702	12.9	714	1 S31502	NADPH-ferrithemopro
22	684.5	12.5	662	2 G88451	protein K102.6 [1
23	683.5	12.5	1147	1 I56375	nitric-oxide synth
24	679	12.4	1429	2 JN0609	nitric-oxide synth
25	678	12.4	1429	2 S16233	nitric-oxide synth
26	677.5	12.4	1147	1 S38253	nitric-oxide synth
27	675.5	12.4	1147	1 I53165	nitric-oxide synth
28	675.5	12.4	1147	2 JC5029	nitric-oxide synth
29	675	12.4	1433	2 G01946	nitric-oxide synth

ALIGNMENTS

RESULT 1

A34286

NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium
N;Contains: NADPH-ferrithemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (C;Species: Bacillus megaterium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: A34286; S43653

R;Ruettinger, R.T.; Wen, L.P.; Fulco, A.J.

J. Biol. Chem. 264, 10987-10995, 1989

A;Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-

A;Reference number: A34286; MUID:89291834; PMID:2544578

A;Accession: A34286

A;Molecule type: DNA

A;Residues: 1-1049 <RUE>

A;Cross-references: GB:J04832; NID:g142797; PIDN:AA87602.1; PID:g142798

R;Munro, A.W.; Lindsay, J.G.; Coggin, J.R.; Kelly, S.M.; Price, N.C.

FEBS Lett. 343, 70-74, 1994

A;Title: Structural and enzymological analysis of the interaction of isolated domains

A;Reference number: S43653; MUID:94215710; PMID:8163021

A;Accession: S43653

A;Molecule type: protein

A;Residues: 430-439;441-496 <MUN>

C;Genetics:

A;Gene: CYP102

C;Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin

C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met

F;262-423/Domain: cytochrome P450 homology <P45>

F;483-1046/Domain: NADPH-ferrithemoprotein reductase homology <FEH>

F;485-622/Domain: flavodoxin homology <FLX>

F;401/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 5457; DB 1; Length 1049;

Best Local Similarity 100.0%; Pred. No. 3.1e-298;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPQKTFGELKNPLINTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60

Db 2 TIKEMPQKTFGELKNPLINTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61

Qy 61 ACDESFPDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMGYHAMV 120

Db 62 ACDESFPDKNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMGYHAMV 121

Qy 121 DIAVOLVQWERNLNADEHIEVPEDMTLTDITGLCGFNYSFVDPQHPFTSMVA 180

Db 122 DIAVOLVQWERNLNADEHIEVPEDMTLTDITGLCGFNYSFVDPQHPFTSMVA 181

Qy 181 LDEAMNKLQANPDDPAYDENKQFOEDIKVMDLVKIIADRKASGEQSDLLTHMLNG 240

Db 182 LDEAMNKLQANPDDPAYDENKQFOEDIKVMDLVKIIADRKASGEQSDLLTHMLNG 241

Qy 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 300

|||||
242 KDPTGEPDDEIRYQITFTIAGHETTSGLLSPALYLVNPNHVLQKAAEAAARVLD 301
QY PVPYSQVQKLVGVNVLNLEALRLWTPAFSLYAKEDTVLGGEYPLEKGDMLVLIPOI 360
Db PVPYSQVQKLVGVNVLNLEALRLWTPAFSLYAKEDTVLGGEYPLEKGDMLVLIPOI 361
QY HRDKTIWGDVVEEFPREFENPNSAIPQAFKPFNGQORACIGQGFALHEATLVLMMLKH 420
Db HRDKTIWGDVVEEFPREFENPNSAIPQAFKPFNGQORACIGQGFALHEATLVLMMLKH 421
QY FPFEDHTNVELDIKETLTLPKPGFVVKAKSKKIPGLGIPSPSTESAKKVRKAENAHNT 480
Db FPFEDHTNVELDIKETLTLPKPGFVVKAKSKKIPGLGIPSPSTESAKKVRKAENAHNT 481
QY PLVLVYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIYVTSNGHP 540
Db PLVLVYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIYVTSNGHP 541
QY PNAKQFVDMVLDQASADEVKGVRYSVFGCGDKNMTATYQVPAFIDETLAAGAENIADR 600
Db PNAKQFVDMVLDQASADEVKGVRYSVFGCGDKNMTATYQVPAFIDETLAAGAENIADR 601
QY GADASDDPEGTYEWRHMSDVAAYFNLDIENSDNKSTLSLQFVDSAAAMP LAKMHG 660
Db GADASDDPEGTYEWRHMSDVAAYFNLDIENSDNKSTLSLQFVDSAAAMP LAKMHG 661
QY AFSTNVVSKELQOQPGSARSSTRHELELPKEASYOEGDHLGVIPRNYEGIVNRVYARFGL 720
Db AFSTNVVSKELQOQPGSARSSTRHELELPKEASYOEGDHLGVIPRNYEGIVNRVYARFGL 721
QY DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPKHVEL 780
Db DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPKHVEL 781
QY EALLEKQAYKEQVLAARLTMLLEKYPACEMKSEFFIALLPISIRPRYISISSPRVDBK 840
Db EALLEKQAYKEQVLAARLTMLLEKYPACEMKSEFFIALLPISIRPRYISISSPRVDBK 841
QY QASITVSVYSGAWSGYGYKGIASNYLAELQEGDTITCFSTPOSEFTLPKDPETPLIM 900
Db QASITVSVYSGAWSGYGYKGIASNYLAELQEGDTITCFSTPOSEFTLPKDPETPLIM 901
QY VPGGTGVAPFRGVQARKQKQOGSLGSAHLYFCGRSPHEDYLYQOEELENAQSEGIITL 960
Db VPGGTGVAPFRGVQARKQKQOGSLGSAHLYFCGRSPHEDYLYQOEELENAQSEGIITL 961
QY HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db HQVSEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 2

D69799
cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Accession: D69799
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.: Bron, S.; Brouillet, C.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, M.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toqnoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Damchin, A.
A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69799
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1061 <KUN>
A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g26330
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeto
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein
F:264-425/Domain: cytochrome P450 homology <P45>
F:493-1057/Domain: NADPH-ferrihemoprotein reductase homology <FHF>
F:495-632/Domain: flavodoxin homology <FLX>
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 60.7%; Score 3314; DB 2; Length 1061;
Best Local Similarity 59.5%; Pred. No. 5.7e-178;
Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

QY 5 MPQPTFGELKPLNTDKPVQALMKIADELGEIFKEAPGRVTRYLSSQRLKEACDE 64
Db 7 IPQPTFGPLGNLPIDKDKPTLSLKLAEEGPIFIHTPAGTIVTSSGHELKVECD 66
QY 65 SRFDNLSQALKFVRDFAGDGLFTSWTHKKNWKAHNLIPFSQAMKGYHAMVDAIV 124
Db 67 ERFDSIEGALKVRAFSGDGLFTSWTHKKNWKAHNLIPFSQAMKGYHAMVDAIV 126
QY 125 QLVQKWERLNADHELEVPEDMTLRLDTIGLCGYNRNSFYRSDPPHPTTSMWRALDEA 184
Db 127 QLIQKWARLNADHELEVPEDMTLRLDTIGLCGYNRNSFYRSDPPHPTTSMWRALDEA 186
QY 185 MNKLQANPDDPAYDENKQFQEDIKVNDLVYKTIADRKASGEQSD-DLLTFHMLNGDP 243
Db 187 MHQQLRVQDKLWRTKQFQEDIKVNDLVYKTIADRKASGEQSD-DLLTFHMLNGDP 246
QY 244 ETGEPLDDENIRYQITFTIAGHETTSGLLSPALYLVNPNHVLQKAAEAAARVLDV 303
Db 247 ETGEKLDDEIRYQITFTIAGHETTSGLLSPALYLVNPNHVLQKAAEAAARVLDV 306
QY 304 SYKQVQKLVGVNVLNLEALRLWTPAFSLYAKEDTVLGGEYPLEKGDMLVLIPOIHRD 363
Db 307 TYKQVLELYIMILNLSRLWTPAFSLYAKEDTVLGGEYPLEKGDMLVLIPOIHRD 366
QY 364 KTIWGDVVEEFPREFENPNSAIPQAFKPFNGQORACIGQGFALHEATLVLMMLKHDF 423
Db 367 RDWKGDAEEFPERFEHQDQVPHAYKPFNGQORACIGQGFALHEATLVLMMLKHDF 426
QY 424 EDHTNVELDIKETLTLPKPGFVVKAKSKKIPGLGIPSPSTESQSA---KVRKAENA--- 477
Db 427 IDHENYELDIKETLTLPKPGFVVKAKSKKIPGLGIPSPSTESQSA---KVRKAENA--- 486
QY 478 --HNTPLLVYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIYVTS 535
Db 487 GLNNRPLLVYSGDGTAGVARELADTASLHGVTKTAPLNDRIGKLPKEGAVIVTSS 546
QY 536 YNGHPDPAKQFVDMVLDQASADEVKGVRYSVFGCGDKNMTATYQVPAFIDETLAAGA 595
Db 547 YNGKPPSNAGQFVQMLQKPELGSHVAVFGCGDHNWASTYQVVPFRFIDQLAEKAT 606
QY 596 NIADRGADADDFTGTYEWRHMSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAAAMP 654
Db 607 RFSARGEVDGDFEGQDGLDEKWSMDAIAKFALELNENADKERSTLSLQFVGRIGESP 666
QY 655 LAKMHGAFSTNVVSKELQOQPGSARSSTRHELELPKEASYOEGDHLGVIPRNYEGIVNRV 714
Db 667 LARSVEASHASTAENRELQSDSDSTRHELELPKEASYOEGDHLGVIPRNYEGIVNRV 726
QY 715 TARFGLDASQQLRLAEAEKLAHLPLAKTVSVEELLQV-VELQDPVTRTQLRAMAAKTVC 773

Db 727 LHREGLRGDTQVTLSSAGRSAGHPLGRPVSLHLLSYSEVQEAATRAQIRELASFVC 786
 Qy 774 PPHKVELEALLEKQAYEQLAKELTLMLELLEKYPACEMKFSFIALPRLPRYYISS 833
 Db 787 PPHRELEELSAEGVYQELKKRISMDLLEKYEACDMFERLELLRLPKPRYYISS 846
 Qy 834 SPRVDEKOAISITVSVSGEAWSGYGEYKGIASNYLAELQEGDTTCFISFQSFETLPKD 893
 Db 847 SPRVNPQASITVGVGRPAWSGRGEYRGVNASNDLAERAGDDVVMFIRPESRFQPKD 906
 Qy 894 PETPLIMVGCTGVAPRGFVQARKQKQEGOSLGEAHLFGCRSPHEDLYSBELENAQ 953
 Db 907 PETPLIMVGCTGVAPRGFVQARKQKQEGOSLGEAHLFGCRSPHEDLYSBELENAQ 965
 Qy 954 SEGIITLHTAFSRMPNQPKYVQHVMEQDQKLELLELDQGAHFYICGDSGOMAPVATL 1013
 Db 966 KDGIVTVHTAFSRKEGMPKYVQVHLMADQADTLISILDRGRLYVCGDSGMAPDVEAL 1025
 Qy 1014 MKSVADYHVQSEADARLWLOOLEEKGRYAKDVWAG 1048
 Db 1026 QKAYQAVHGTGCEQAQNLRLHLDQTMGYAKDVWAG 1060

RESULT 3

A:69975
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus subtilis
 N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 1.10.3.3)
 C:Species: Bacillus subtilis
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Jun-2002
 C:Accession: A69975
 R:Kunst, F.; Ogasawara, N.; Möszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortel, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodura, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtschappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Laubers, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M. Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: A69975
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1054 <KUN>
 A:Cross-references: GB:299117; GB:AL009126; NID:g2634966; PID:g2635162
 A:Experimental source: strain 168
 A:Genetics:
 C:Gene: yrbH
 C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin homology
 C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; monooxygenase; oxidoreductase
 F:486-1050/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:486-625/Domain: flavodoxin homology <FLX>
 F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 60.1%; Score 3281.5; DB 1; Length 1054;
 Best Local Similarity 58.5%; Pred. No. 3.8e-176;
 Matches 614; Conservative 173; Mismatches 254; Indels 9; Gaps 6;
 Qy 5 MPQKRTGELKNLPLNDRPQVQMLKIADELGFKEPAPGRVTRVYLLSRLRKEACDE 64
 Db 7 IPQPKTYGPKLPHLEKEQLSQSLWIRIADLDELGFKEPAPGRVTRVYLLSRLRKEACDE 66
 Qy 65 SRFDKNIQALKVDFRDFAGDLFTSWTHEKNWKAHNLILLPSFSQQAQKGYHAMVDIAV 124
 Db 67 KRFDKNLGLKQKREFGGDLFTSWTHEPNWQKAHLLRLLPSFSQQAQKGYHAMVDIAV 126

Qy 125 QLQKWERLNADEHIEVPEDWTRTLTDTIGLCGFNYRFSFYRDPHPFITSMVALDEA 184
 Db 127 QLQKWERLNADEHIEVPEDWTRTLTDTIGLCGFNYRFSFYRDPHPFITSMVALDEA 186
 Qy 185 MNKLQORANPDNDAYDENKROFQEDIKVNDLVKIIADKASGEQS--DLLTHMLNKDP 243
 Db 187 MNOSKRGLQDKMKVTKLQFKDIEVMSLVDRMIAERKANPDENKDLSSLMLYAKDP 246
 Qy 244 ETGEPDLDENIRYQIITFLAGHETTSGLLSFALYFLVKNPHVLOKAAEAARLVDPVP 303
 Db 247 VTGETLDDENIRYQIITFLAGHETTSGLLSFALYFLVKNPHVLOKAAEAARLVDPVP 306
 Qy 304 SYQVQKOLKYGVMVNLNEALRLMPTAPAFSLYAKEDTVLGGYPLEKEGDELMLVLIQHRD 363
 Db 307 EYKIQLOLKIRYMLNETLRLYPTAPAFSLYAKEDTVLGGYPLEKEGDELMLVLIQHRD 366
 Qy 364 KTWGDVDEFRPERFENPSAIPQAFKPGNGORACIGQOFALHEATLVLMGLMKHDF 423
 Db 367 QNAGWPAEDFRPERFENPSAIPQAFKPGNGORACIGQOFALHEATLVLMGLMKHDF 426
 Qy 424 EDHTNYELDIKETLTLKPEGVVRAKSKKTIPLGIPSPSTEQS---AKKVRKKAENAHNT 480
 Db 427 INHTGYELKIKEALTIKPDDEKITVPRK--TAAINVQKEQADIKAEKPKETPKHGT 484
 Qy 481 PLLVLYGSNMGTAEGTARDLADIAMSGFAPQVATLDSHAGNLREGAVLIVTASYNGHP 540
 Db 485 PLLVLYGSNMGTAEGTARDLADIAMSGFAPQVATLDSHAGNLREGAVLIVTASYNGHP 544
 Qy 541 PDNAKQFVDWLQASADEVKGVRYSVFCGCKNWTYQKVPFIDETLAAGAENTADR 600
 Db 545 PDNAAGFVWLKELEGQLKGSYAVFCGCKNWTYQKVPFIDETLAAGAENTADR 604
 Qy 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMLAKMHG 660
 Db 605 GEGDAADDFESHRESWENRWEKTMDFADINEIAQEDRPSLSITFSEATETPVAKAYG 664
 Qy 661 AFSTNVVASKELQPGSARSTRHLEIELEPKPEASTQEGDHLGVIPRNVEGIVNVRTARFGL 720
 Db 665 AFEIGVLENRELOTAASTRSTRHLEIELEPKPEASTQEGDHLGVIPRNVEGIVNVRTARFGL 724
 Qy 721 DASQOIRLEAEEELKHLPLAKTYSVRELL--QYVELODPVTRTOLRAMAAKTVCPPHKVE 779
 Db 725 QSNHVIKSSGAH--MAHLMDPRPIKVVLDLSYVELQEPASRLQRELASTVCPPHOKE 783
 Qy 780 LEALLERQQA--YKEQVLAKRITMLELLEKYPACEMKFSFIALPRLPRYYISSSPRVD 838
 Db 784 LEQLVSDGDIYKEQVLAKRITMLELLEKYPACEMKFSFIALPRLPRYYISSSPRVD 843
 Qy 839 EKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTTCFISFQSFETLPKDPEPL 898
 Db 844 ANIVSMTVGVVYKASAWSGRGEYRGVNASNYLAELNTGDAACFIPTQSGFQMPNDPPTM 903
 Qy 899 IMVGPCTGVAPRGFVQARKQKQEGOSLGEAHLFGCRSPHEDLYSBELENAQSEGLI 958
 Db 904 IMVGPCTGVAPRGFVQARKQKQEGOSLGEAHLFGCRSPHEDLYSBELENAQSEGLI 963
 Qy 959 TLHTAFSRMPNQPKYVQHVMEQDQKLELLELDQGAHFYICGDSGOMAPVATLMSYA 1018
 Db 964 TIRRCYSRVENEPKGYVQVHLLKQDTQKMLTLEKGAHIIYVCGDSGOMAPDVERTLRUAYE 1023
 Qy 1019 DVHQVSEADARLWLOOLEEKGRYAKDVWAG 1048
 Db 1024 AEKAASQESAVWLQKLDQRRYKDVWAG 1053

RESULT 4

RDRT04
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rat
 N:Alternate names: NADP-cytochrome P450 reductase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Jun-2002
 C:Accession: A36073; A00402; A25813
 R:Porter, T.D.; Beck, T.W.; Kasper, C.B.

Biochemistry 29, 9814-9818, 1990
A:Title: NADPH-cytochrome P-450 oxidoreductase gene organization correlates with structure
A:Reference number: A36073; MUID:91104880; PMID:2125483
A:Accession: A36073
A:Molecule type: DNA
A:Residues: 1-678 <P02>
A:Cross-references: GB:J05291
R:Porter, T.D.; Kasper, C.B.
Proc. Natl. Acad. Sci. U.S.A. 82, 973-977, 1985
A:Title: Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductase cDNA and
A:Reference number: A00402; MUID:85140278; PMID:3919392
A:Accession: A00402
A:Molecule type: mRNA
A:Residues: 1-678 <P0R>
A:Cross-references: GB:M10068; NID:g203872; PIDN:AAA41064.1; PID:g203873
R:Murakami, H.; Yabusaki, Y.; Ohkawa, H.
DNA 5, 1-10, 1986
A:Title: Expression of rat NADPH-cytochrome P-450 reductase cDNA in Saccharomyces cerevisiae
A:Reference number: A25813; MUID:86163762; PMID:3082610
A:Accession: A25813
A:Molecule type: mRNA
A:Residues: 1-678 <MUR>
A:Cross-references: GB:M12516; NID:g203878; PIDN:AAA41067.1; PID:g203879
C:Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of FMN
and to bacterial flavodoxins.
C:Genetics:
A:Introns: 60/2; 76/3; 119/3; 169/3; 211/2; 241/2; 313/2; 353/1; 413/3; 463/3; 553/3; 593/3
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; membrane protein
F:1-56/Domain: membrane-bound #status predicted <MEM>
F:77-227/Domain: FMN binding #status predicted <FMN>
F:80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:82-224/Domain: flavodoxin homology <FLX>
F:84-95/Region: FMN-phosphate binding #status predicted
F:267-326/Domain: FAD binding #status predicted <FAD>
F:293-296/Region: FAD-pyrophosphate binding #status predicted
Query Match 14.2%; Score 777.5; DB 1; Length 678;
Best Local Similarity 32.2%; Pred. No. 6.4e-36;
Matches 211; Conservative 111; Mismatches 263; Indels 71; Gaps 23;

QY 444 FVYKAKSKTIP-----LGGIPSPSTEQS-AKKVKKKAENAHNTPLLVLYGSGNMGTAAGTAR 498
DB 42 FIFRKKKEELPEPSKLTAPPVKESFVEKKMKTKGRN-----IIVFGSQTGTAEFAN 96
QY 499 DLADIAMSKGEAPQVATLDLSDH-----AGNLPKPR--EGAVLIVTASY-NGHPPDNAAQFVDWL 551
DB 97 RLSKDAHRYGMRGMSADPEYDLADLSSLPEDKSLVFCMATYGGEDPTDNDQDFYDNL 156
QY 552 DQASADEVKGVRYSVFCGDKNWTYQKVA---FIDETLAAGAENIADGEADSD 608
DB 157 QETDQVD-LTGKFAVFLGNK-----TYEHFNAMGKYVDQRLQGLGAORIFELGLGDDGN 211
QY 609 FECTYEERHMHMSDVAAYFNLDIENSDNKSLSLQFVDSADMPKAKH----- 659
DB 212 LEEDFTWRFQFPAVCEFFGVEATGEESIRQYELVWHE---DMQVAVYTGEMGRKLS 268
QY 660 -----GAFSTNVYASKELOQPGSARSTRHLEIEL-PKEASVQEGDHLGVIPRNY 707
DB 269 YENQKPPFDKAPFLAAVTANRKLQ-GTERHLMHLELSDSKIRYSGDHVAVYPAND 327
QY 708 EGVNVRNTRFQ---LDASQOIRLEAEKEHLAHLPLAKTVSVELLYQVLOQDPVTRQLR 765
DB 328 SALVNOIGETLGADLVIMSLNLDSESNKHPFPCTTYRTALTYYLDTITNP-PRTNVL 386
QY 766 AMAAKTVCP-----HKVELEALLKQAYKQVLAKRITLMLELLEKYPACEMKSEFTA 819
DB 387 YELAQVASESEGEHLKMKASSGEGEKLYLSNVVBARHILAILQDPSLRPPIDHLC 446
QY 820 LLPSIIRPYISISSPRVDKQASITVSVVSGEANSVGEYKGIASNYL-AELQEGDT-- 876
DB 447 LLPRLQARYSIASSSKVHPNSVHICAVAVEYEAKSGRYN-KGVATSWLRAKEPAGENG 505

877 ---ITCFISTPQSEFTLPKDPETPLIMVPGTGVAPPRFVQARKOLKEQOSLSGAHLY 933
DB 506 RALVPMFVR--KQFRLPFKSTTFVIMVGGTGIAPFMGFIQERAWLREQCKEVEGTELLY 563
QY 934 FGRSPHEDYLYOELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVNEQDGKLLIELDQ 992
DB 564 YGCRSDEDELYREELARPHKDGALQTNVAFSR-EQAHKVYVQVHLLKRDREHLWLKLIHE 622
QY 993 -GAHFYICGDSOMAPAVEATLMKSVADYHVSSEADARLWLOLEKRGYAKDYWA 1047
DB 623 GGAHYVCGDARNMAKDQVNTFYDVAEFGPMHTQAVDYVKKLMTKRGYSLDVWS 678

RESULT 5
RDPG04
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig
N:Alternate names: NADP-cytochrome P450 reductase
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 04-Dec-1986 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C:Accession: A25584; A00403
R:Hanlu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.
Biochemistry 25, 7906-7911, 1986
A:Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcine
A:Reference number: A25584; MUID:87101085; PMID:3099837
A:Accession: A25584
A:Molecule type: protein
A:Residues: 1-677 <HAN>
R:Voegel, F.; Lumper, L.
Biochem. J. 236, 871-878, 1986
A:Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome
A:Reference number: A00403; MUID:87075664; PMID:3098240
A:Accession: A00403
A:Molecule type: protein
A:Residues: 56-162 'S', 164-173 'D', 175-338 'A', 340-377 'D', 379-399 'E', 401-445 'L', 44
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem
C:Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav
F:76-126/Domain: FMN binding <FMN>
F:79-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:81-223/Domain: flavodoxin homology <FLX>
F:451-476/Domain: FAD binding <FAD>
F:1/Modified site: acetylated amino end (Gly) #status experimental

Query Match 14.1%; Score 769; DB 1; Length 677;
Best Local Similarity 31.9%; Pred. No. 1.9e-35;
Matches 224; Conservative 109; Mismatches 275; Indels 94; Gaps 27;

QY 401 IQQFALHEAT-----LVGLMKLKHDFEDHTNY---ELDIKETLT-LKPEGFVYKAKS 450
DB 15 VAEVSLFSATDMVLSLVGLLTYWIFPRKKKDEYEPFSKTIETTTSSVKDSFV----- 69
QY 451 KKIPLGGIPSPSTEQSAAKVRKKAENAHNTPLLVLYGSGNMGTAEGTARDLADIAKSGFA 510
DB 70 -----EKMKTKGRN-----IIVFGSQTGTAEFANRLSKDAHYGMR 107
QY 511 PQVATLD-----SHAGNLPKPR-EGAVLI-VTASY-NGHPPDNAAQFVDWLQASADEYKGVYR 563
DB 108 GMAADPEEYDLSDLSLPEIENALAVFCMATYGGEDPTDNDQDFYDMLQADVD-LTGK 166
QY 564 YSVFCGDKNWTYQKVA---FIDETLAAGAENIADGEADSDDECTYEWEHEM 620
DB 167 YAVFLGNK-----TYEHFNAMGKYVDKRLQGLGAORIFDLGLGDDGDNLEEDFITWREF 222
QY 621 WSDVAAYFNLDIENSDNKSLSLQF-----VDSAA-----DMPLAKMHGAFS 663
DB 223 WPAVCEHFGVEATGEESIRQYELVWHTDMTAVVYTGEMGRKLSYENQKPPFDKAPNPL 282
QY 664 TNVASKELQPGSARSTRHLEIEL-PKEASVQEGDHLGVIPRNVETGVNRTARGLDA 722
DB 283 AVYTTNRKLQ-GTERHLMHLELSDSKIRYSGDHVAVYPANDSALYNQLGILGTDL 341
QY 723 SQOI---RLEAEKEHLAHLPLAKTVSVELLYQVLOQDPVTRQLRAMAAKTVCPKHYE 779
DB 342 DIVMSLNLDSESNKHPFPCTTYRT-ALTYLDTITNPRTNVLYELAQYASESESEQ 400

[illegible]

Dn
212 NLEEDITWREQTPAVCEHFGVYATGESSIRQVELVL---HTDIDVAKYOGEMGRLK 268

Qy
660 -----GAFSTNVVASKELOQGPGSARSTRHLIEL-PKEASYQEGLHGIVPRN 706

Dn
269 SYENQKPPFDAPKNPFLATVTNTKLNQ-GTERHLMHLELSDSKIRYESGDHVAVVPAN 327

Qy
707 YEGIVNRVTRFCLDASQQI--RLBAEEELKAHLPL-----AKTVSV 746

Dn
328 DSAIVNLQGLEIGADLDVVNSLNNDESNKKHPFCPTSYRYALTYLLDITNPRTNVL 387

Qy
747 EELLQYVELODPVRTQLRAMAAKTVCPPHKVLEALELKEOAYKEQYLAKRLTMLELEEK 806

Dn
388 YELAQA--ADPAEQEQLRKMASSSG-----EGKELYLSWWVEARRHILATIQQ 434

Qy
807 YPACMKFEFFIALPSIPRYSISSSPRVDEKQASITSVVSVEAWSGYGVKGIAVN 866

Dn
435 YPSLRPDIDLCELLPLQARYTSASSSKVHNPNSHVICAVAVEYTEKAGRLN-KGVATS 493

Qy
867 YL-AELQEGDT----ITCFISTPQSSEFTLPKDPEPLIMVGPGTGVPAPRGVFQARKOL 920

Dn
494 WLRAKEPAGCGRALVPMFVR--KSQFLRPFRATTPIVMVGPGTGVPAPRGFIQRRAWL 551

Qy
921 KEQGOSLGIEAHLYFGCRPHEDLYIOBELENASEGIIT-LHTAFSRMPNQPKTYVOHYM 979

Dn
552 RQDGKEVGETLLYYGCRRRAEDLYRELAGFKDKGTLSQLNFASFREQAQ-KVIYQHLL 610

Qy
980 EQDGKLIELDD-GAHFYICGGSGOWAPAEATLMKSYADVHOVSSEADRWLQOLEEK 1038

Dn
611 RRDKHLWRLIHEGGHHIYVCGDRNKARDVQNTFYDIYAELGAMEHAQVDYVKMLTK 670

Qy
1039 GRYAKDVWA 1047

Dn
671 GRYSLDWS 679

RESULT 7

A60557

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - human

N;Alternate names: NADP-cytochrome P450 reductase

C;Species: Homo sapiens (man)

C;Date: 17-Apr-1993 #sequence revision 31-Dec-1993 #text_change 03-Jun-2002

C;Accession: A33421; A60557; S21686

R;Hanlu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.

Biochemistry 28, 8639-8645, 1989

A;Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from

A;Reference number: A33421; PMID:90105390; PMID:2513880

A;Accession: A33421

A:Molecule type: protein

A;Residues: 2-677 <HAN>

A;Note: 551-Gln was also found

R;Yamano, S.; Aoyama, T.; McBride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J.

Mol. Pharmacol. 36, 83-88, 1989

A;Title: Human NADPH-P450 oxidoreductase: complementary DNA cloning, sequence and vac

A;Reference number: A60557; PMID:89313720; PMID:2501655

A;Accession: A60557

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-137,'G','A',39-577,'DV',580-677 <YAM>

R;Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.

Arch. Biochem. Biophys. 294, 168-172, 1992

A;Title: Quantification of cytochrome P450 reductase gene expression in human tissues

A;Reference number: S21686; PMID:92198003; PMID:1550342

A;Accession: S21686

A:Molecule type: mRNA

A;Residues: 2-493,'Y',501-517,'L',519-536,'WH',539-677 <SHE>

A;Cross-references: GB:S90469; NID:g247306; PIDN:AAB21814.1; PID:g247307

C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo

C;Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav

F;1-56/Domain: membrane-bound #status predicted <MEM>

F;2-677/Product: NADPH-ferrihemoprotein reductase #status experimental <MAT>

F;77-227/Domain: FMN binding #status predicted <FMN>

F;80-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

Db 630 YIYCGDAKMARDVHRLHTIAEQGALDSSKRAESWYKNLQMTGRYLRDVW 681

030 111 CGDARGMARDVHMLPHI IAVEQ6ALDSSAGHESWVRNLTQMIGALILADVM 000

RESULT 11

A56592
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - house fly
N:Alternate names: NADPH-cytochrome P450 reductase; P450 reductase
C:Species: Musca domestica (house fly)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 03-Jun-2002
C:Accession: A56592
R:Koener, J.F.; Carino, F.A.; Feyerelsen, R.
Insect Biochem. Mol. Biol. 23, 439-447, 1993
A:Title: The cDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reductase
A:Reference number: A56592; MUID:93284260; PMID:8508186
A:Accession: A56592
A:Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-671 <KOE>
A:Cross-references: GB:119897; NID:G308945; PID:AAA29295.1; PID:G308946
A:Note: sequence extracted from NCBI backbone (NCBIN:134359, NCBIN:134361, NCBIN:133605)
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; membrane protein; NADP; oxidoreductase
F:77-669/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:79-221/Domain: flavodoxin homology <FLX>

Query Match 13.5%; Score 735.5; DB 2; Length 671;
Best Local Similarity 30.0%; Pred. No. 1.4e-33;
Matches 199; Conservative 123; Mismatches 255; Indels 87; Gaps 25;

QY 444 FVYAKSKKIPIGG-----IPSPTEQSA--KKVRKKAENAHNTPLLVXGNNMGTA 494
DB 35 FMRSRKKKEAPIRSYSIQPTTVSTVSTTENSFIKLLK-----ASGRSLVVFYGSQTGTA 89
QY 495 GTARDIADAM---SKGFA--QVATLDS--HAGNLPREGAVLIVTASTNGHPPNAKOF 547
DB 90 EFAGRLAKELRYRMKGWADVPECDMEELLQMDIPNSLAVFLCYATYGEQDPTNAMEF 149
QY 548 VDWLQASADEKGVYRVSVEGCGKNWATYQKVPAFIDETLAAGAENIADRGADSD 607
DB 150 YEWITNGEVD--ITGLNAYVGLGNKY--EYHNKVALYVDKRLLEELGATVFEGLGDDDA 207
QY 608 DFEQTYEWEHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP-----LAKMH- 659
DB 208 NIEDDFTWKDFWPSVCFDFG--IEGSGEVLWRFLELQPDVQPDRIYTGTEIARLHS 265
QY 660 -----GAFSTNVASLQOPGARSATRHLEIEP--KEASYQEGDHLGVIPRY 707
DB 266 MQNQRPFPDAKNPFLASVINRELHK--GGGRSCMHIELDIGSKRYDAGDHIAFYPI 324
QY 708 EGVNVRV--TAREGLD--ASQQLRLEAEKLAHLP-----LAKTVSVE 747
DB 325 KILVEKLGKLDANLDTVESLINTDSSKKHPPFPCTTYRTALHYLEITAIPTHTLHK 384
QY 748 ELQVYELQDPVTRTQLRAMAARTVCPPHKVEALELLEKQAYKEQVLAKRLTLMLELKY 807
DB 385 ELAEY--CSDEKDKFELRNASTI--PE-----GREKYQNQIONSSRNIVHLEDI 431
QY 808 PACEMKFSEFIALLPSIRPRYSISSPPVDEKQASITVSVSGEAWSGYGEYKIASNY 867
DB 432 KSCRPPIDHICELLRLQPRYSISSSKSLYPTNWHITAVLYQVETPTGRVN--KGATSY 490
QY 868 LAELQD--GDT--ITCFISTPQSEFTLPKDPETPLIMVPGTGVAPRFGVQARKOLKEOG 924
DB 491 MKEKNPSGEVKNPVFIR--KSQFLPTKSEIPIIMVPGTGLAPFRGIQRFQRLROG 548
QY 925 QSLGEAHLVFGCRSPHEDLYQGELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGK 984
DB 549 KVVGDITLYFGCRKKDEDFIYREELEQYVQNGTFLTKTAFSR--DQEKIYVTHLIEQDAD 607
QY 985 KLIELL--DQGAHFYICGDSQAPAVEATLMKSYADVHOVSEADARLWLOOLEEKGRTAK 1043
DB 608 LIWKVIGEQGHFYICGDAKNMAVDVNRILVILSTLKGNNMESDAVQYIKKMEAKRYSA 667
QY 1044 DYWA 1047
DB 668 DWWS 671

RESULT 13

A47298
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - mung bean
N:Alternate names: NADPH-cytochrome P450 reductase

RESULT 12

A28577
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - brown trout (fragments)
C:Species: Salmo trutta (brown trout)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 03-Jun-2002
C:Accession: A28577
R:Urenjak, J.; Linder, D.; Lumpert, L.
J. Chromatogr. 397, 123-136, 1987
A:Title: Structural comparison between the trout and mammalian hydrophilic domain of
A:Reference number: A28577; MUID:88008061; PMID:3116019
A:Accession: A28577
A:Molecule type: protein
A:Residues: 1-601 <RUE>
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F:25-599/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:27-169/Domain: flavodoxin homology <FLX>

Query Match 13.2%; Score 723; DB 2; Length 601;
Best Local Similarity 30.2%; Pred. No. 6.1e-33;
Matches 195; Conservative 106; Mismatches 239; Indels 106; Gaps 21;

QY 459 PSPSTEQSA--KKVRKKAENAHNTPLLVYGSNMGTAEATARDLADIAKSKGFAPQVATL 516
DB 5 PAPSTQETSFIEKMKTKGRN-----IVFYGSQTGTGEEFANRLSKDAHRYGMSGNAADP 59
QY 517 D-----SHAGNLPREGAVLIV--TASY--NGHPDPNKAQFVDMWLDQASADKVGVRYSVFGC 569
DB 60 EYDMSLSRLAEIGNSLAIFCMATYEGDPDYNADQFYDWL--QETDGLSGVNYVPFAL 118
QY 570 GDNKWTATYQKVPAFIDETLAAGAENIADRGADSDDEFGTYEWEHMSDVAAYFN 629
DB 119 GDKTY--EYHNAGAYVDKLEELGAKRVEDLGMGDDGDNLEEDFTWTROQFWPAMEHFG 177
QY 630 LDENSEDNKSTLSLQFVDSAADMPLAKMH-----GAFSTNVAS 669
DB 178 VEASGDSVSRQYELK---EHNDINMKNVYTGELGRKLSFETQKPPDPAKPNFLADPTVN 234
QY 670 KELQPGSARSATRHLEIEP--KEASYQEGDHLGVIPRYEGIVNRTARFGLDASQIIRL 728
DB 235 RKLKAGELHK--MHLEVDITGSKIRYESGDHVAVPTNNTVINRUGQILGVDLDSVISL 293
QY 729 EAEK-----LAHLAKTASVEELQY--VELQDPVTRTQLR 765
DB 294 NNLDESNKKHPPFPCTTYRTALTHTYLDIHP--RTNVLVELAQYATDLKQENWDSMA 351
QY 766 AMAATVCPPHKVEALELLEKQAYKEQVLAKRLTLMLELLEKYPACMKFSEFIALLPSIR 825
DB 352 SSAPE-----GKALYQSFVLEDRNLTALILEDLPRLPPIDHLCCLMPLRQ 397
QY 826 PRYISISSPPVDEKQASITVSVSGEAWSGYGEY--KGIASNYLAELQEGDTITCFIST 883
DB 398 ARYISASSKVVHPNSIHICAVLV-----EYTKGVATVTLKYLIR----- 437
QY 884 PQSEFTLPKDPETPLIMVPGTGVAPRFGVQARKOLKEQSGSLGEGAHLYFGCRSPHEDY 943
DB 438 -KSQFLRFPKNSPVMVPGTGVAPRFGVQARKOLKEQSGSLGEGAHLYFGCRSPHEDY 946
QY 944 LYQEELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKLL--IELDQGAHFYICGD 1001
DB 497 LYQEELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKLL--IELDQGAHFYICGD 1001
QY 1002 GSQMAPAVEATLMKSYADVHOVSEADARLWLOOLEEKGRTAKDVA 1047
DB 556 ARNARDVQTAPEYAEELGGMTRTQATDIYIKKMTKGRYSQDVWS 601

C;Species: Vigna radiata (mung bean)
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 03-Jun-2002
 C;Accession: A47298
 R;Shet, M.S.; Sathasivan, K.; Arlotto, M.A.; Mehdy, M.C.; Estabrook, R.W.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2890-2894, 1993
 A;Title: Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean.
 A;Reference number: A47298; MUID:93219390; PMID:8464904
 A;Accession: A47298
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-690 <SHE>
 A;Experimental source: var. Berken, microsomes
 A;Note: sequence extracted from NCBI backbone (NCBIP:128723)
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase
 C;Keywords: flavoprotein; NADP; oxidoreductase
 F;80-689/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;84-233/Domain: flavodoxin homology <FLX>

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Query Match      13.2%; Score 723; DB 2; Length 690;
Best Local Similarity 30.6%; Pred. No. 7.5e-33;
Matches 191; Conservative 109; Mismatches 259; Indels 66; Gaps 19;

QY 477 AHTPTLLVYGSNMGTAEGTARDLAD--IAMSFGAPQVATLDSHAGN-----LPREG 527
DB 77 AGTKVTIFGTGTGAEGFAKALAEIKARYEKAAYKVYDLDYAADDDLYEELKKES 136

QY 528 AVLIVTASY--NGHPPDNNAKQFVDWLQASDA---VKGVRYSVFGCGDKNWTYQKQVPA 583
DB 137 LVFFMLATYGDGEPTDNNARFYKFWTEGDKRGWLGKLYGVFGLGNROY--EHNKIGK 195

QY 584 FIDETLAAGAENIADGEADSDDFEGTYEVRHMSDVAAYFNLDIENSEDNKSTLS 643
DB 196 VDDEELAEQAKRLVAVGLGDDQSDIEDDFSANKESLWSELD-----QLLRDEDDANTVS 250

QY 644 LQFVDSAADN-----PLA-----KMGCAFSTNVVASKELQOPGARS 680
DB 251 TPTTAILEYRVVHIDPTASTYDNDNSTVANGNTEFDIHPHPCRVNVAQKELHKPSDRS 310

QY 681 TRHLEIETLP--KEASYQEGDHLGVIPRNYEGIVNRVTRARFGIDASQQTIRLEAEKLAHL- 738
DB 311 CIHLEFDISGTSITDYGHDGVVAENCTEETGKLLQNLDDLFSLHTDKDGTSLG 370

QY 739 -----PLAKTVSYE--ELLQVLELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAY 789
DB 371 GSLPLPPPGCSRLTARADLNNPRKAAALALATH--ASEPSEDERLKLFLSSPQGRDEY 429

QY 790 KEQVLAKRLTMLELLEKYPACEMKSEFI--ALLPSIRPRYSISSSSPRVDEKQASITVS 848
DB 430 SKWVVGQSRLVEVMAEFPSSAKPLGVFFAIAIPLQPRYSISSSSPRFAPQRVHVTCAL 489

QY 849 VSGEAWSGYGEYKGIASNYL-----AELQEGDTITCFSTPQSEFTLPKDPETPLIMVG 902
DB 490 VYGPPTPG--RIHKGVCSTWKNKAIPEKSDCSAPIFIR--PSNFKLPVDHSIPLIMVG 546

QY 903 PGTGVAPFRGTVQARKQKQOSLGEAHLFYGCRSPHEDYLYOELEENASQSGIIT--LH 961
DB 547 PGTGLAPFRGLQERYALKEDGVLGCPALLFFGCRNRQMDFIYEDELKSEVQGSSELI 606

QY 962 TAFSRMPNQPVTYVHVEQDQKLLLELDQGAHFYICGDSOMAPAVEATLMSYADVH 1021
DB 607 VAFSR--EGAKEVYVQHMKDKAHLWSLSIQGGGLYVCGDAKGMDVHRTLHLSIVQEQE 665

QY 1022 QVSEADARLWLOOLEEKGRYAKDVW 1046
DB 666 NVDSTRAEAIVKQLMDGRYLQDVW 690

```

RESULT 14

T10720

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - opium poppy

N;Alternate names: ferrihemoprotein p-450 reductase; NADP-cytochrome reductase

C;Species: Papaver somniferum (opium poppy)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002

C;Accession: T10720
 R;Rosco, A.; Paull, H.H.; Priesner, W.; Kutchan, T.M.
 Arch. Biochem. Biophys. 348, 369-377, 1997
 A;Title: Cloning and heterologous expression of NADPH-cytochrome P450 reductases from Arabidopsis thaliana.
 A;Reference number: Z17096; MUID:98096363; PMID:9434750
 A;Accession: T10720
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-683 <ROS>
 A;Cross-references: EMBL:U67185; NID:g2580496; PIDN:AMC05021.1; PID:g2580497
 C;Function:
 A;Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases;
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase
 C;Keywords: flavoprotein; NADP; oxidoreductase
 F;80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;82-230/Domain: flavodoxin homology <FLX>

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Query Match      13.0%; Score 711.5; DB 2; Length 683;
Best Local Similarity 30.3%; Pred. No. 3.3e-32;
Matches 191; Conservative 113; Mismatches 263; Indels 63; Gaps 20;

QY 470 VRKAENAHNTP-----LLVLYGSNMGTAEGTARDLAD--IAMSFGAPQVATLDSHAG-- 521
DB 64 IDKEEEIEVDPGKIKLTIFGTGTGAEGFAKALAEIKARYKAVKVYDLDYAAED 123

QY 522 ----NLPREGAVLIVTASY--NGHPPDNNAKQFVDWLQD---ASADEVGVRSYVFGCGDKN 573
DB 124 DQYEELKKESLVEFFWVATYGDGEPTDNNARFYKFWTQEHGEGWGLQOLTYGVFGLGNRQ 183

QY 574 WATYQKVPFIDETLAAGAENIADGEADSDDFEGTYEVRHMSDVAAYFNLDIENSEDNKSTLS 623
DB 184 Y-EHFNKIADVBDQLGKQAKRIVQVGLGDDQCIEDDFTAWRELLWTELDQLLKQEDA 242

QY 624 -----VAAYFNLDIENSEDNKSTLSLQFVDSA--ADMPLAKMHGAFSTNVVASKELQ 674
DB 243 APSVATPYIATVPEYRVVIHETVVAALDDKHINTANGDVAFDILHPC--RTIVAQORELHK 301

QY 675 PGSARSTRHLEIETLP--KEASYQEGDHLGVIPRNYEGIVNRVTRARFG--LDSAQOIRLEAE 731
DB 302 PKSDRSCTHLEFDISGSLVATYGDGHVGYVAENCTEETGKLLQNLDDLFSLHTDKD 361

QY 732 EEKLAHLPLAKTVSY-----ELLQVLELQDPVTRTQLRAMAAKTVCPPHKVELEA 782
DB 362 DGS-----PQGSLSPPPPPGFCTLSALARYADLNNPRKASLIASLSHASVPSAEIRLF 417

QY 783 L---LEKQAYKEQVLAKRLTMLELLEKYPACEMKSEFI--ALLPSIRPRYSISSSSPRV 838
DB 418 LSSPLGKNEYSKWVVGQSRLLEIMAEFPSSAKPLGVFFAIAVAPRLPPRYSISSSPKFA 477

QY 839 EKQASITVSVSGEAWSGYGEYKGIASNYLAELQEGDT--ITCFISTPQSEFTLPKDPETP 897
DB 478 PSRIHVTCALVYGSPG--RVHRCVCSWTKMHKAVPQDSWAPIFVYRT--SNFKLPADPSTP 534

QY 898 LIMVPGTGVAPFRGTVQARKQKQOSLGEAHLFYGCRSPHEDYLYOELEENASQSGI 957
DB 535 IIMVPGTGLAPFRGLQERYALKEDGVLGCPALLFFGCRNRQMDFIYEDELNFFVERGV 594

QY 958 IT-LHTAFSRMPNQPVTYVHVEQDQKLLLELDQGAHFYICGDSOMAPAVEATLMS 1016
DB 595 ISELVIAFSR--EGEKEVYVQHMKDKAHLWSLSIQGGGLYVCGDAKGMDVHRTLHTI 653

QY 1017 YADVHVQYSEADARLWLOOLEEKGRYAKDVW 1046
DB 654 AQEQGPMESSAAEAANKLQVEERYLRDVW 683

```

RESULT 15

S37159

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - spring vetch

C;Species: Vicia sativa (spring vetch, tare)

C;Date: 20-May-1994 #sequence_revision 03-Aug-1995 #text_change 03-Jun-2002

R;Benveniste, I.; Begue-Kirn, C.; Lesot, A.; Hasenfratz, M.; Durst, F.

submitted to the EMBL Data Library, September 1993

A:Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P450
A:Reference number: S37159
A:Accession: S37159
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-692 <BEN>
A:Cross-references: EMBL:226252; NID:g400531; PIDN:CAA81211.1; PID:g400532
C:Superfamily: NADPH-ferrithemoprotein reductase; flavodoxin homology; NADPH-ferrithemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F:83-691/Domain: NADPH-ferrithemoprotein reductase homology <FEH>
F:85-234/Domain: flavodoxin homology <FLX>

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Query Match      13.0%; Score 711; DB 2; Length 692;
Best Local Similarity 28.4%; Pred. No. 3.5e-32;
Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

QY 406 ALHEATLVGLMMLKHFDFEDHNYELDIKETLTLPKPGFVVKAKSKKIPLGIGIPSPSTEQ 465
DB 32 ATTSAAVITGLLV--FLMKSPDRSRELRPVTPK---FTVRKHEDDEV----- 76
QY 466 SAKKVRKKAENAHNTPLLVLYGNSMGTAGTARDLAD--IAMSKGFAPOVATLDSHA--- 520
DB 77 -----DRGKTKVTVFYGTGTAGTAEKPAKALAEIKARYEKAVKVVWDMDYVIDD 126
QY 521 ----GNLPREGAVLIVTASY-NGHPPDNAQFVDWLDQASADE---VKGVRYSVFCGDK 572
DB 127 DQVEEKLKKTETLVFFMLATYGDGPTDNaARFVKNFTGEEKRGTLWQLQTYGVFALGNR 186
QY 573 NWATYYQKVPATIDETLAAGAENTADRGADASDDFEGTYEEHREHMMSDVAAYFNLDI 632
DB 187 QY-EHFNKIGKIVDELTQGAARLVPVGLGDDQSDIEDFNWAKETLWPELD-----OL 240
QY 633 ENSDNKSTLSLQFVDSADMPLA-----KMHGAFSTNVVAS 669
DB 241 LRDEDDVNTASTPYTAISEYRVVTHDPTVSPSYENHFNVANGGAVFDIHHPCRVNAVVR 300
QY 670 KELQPGSARSTRHLEIELP-KEASVQEGDHLGVIPRNYEGIVNRVTRARFGLDASQQIRL 728
DB 301 RELHKPQSDRSCITHLEFDLSGTGVYETGDHGVVAENCDETVEEAGKLGQSLDLLFSL 360
QY 729 EAEEEKLAHL-----PLAKTVSVELLQ-VVELQDPVTRTQIRAMAATVCPPHKVELE 781
DB 361 HTDKEDGTSLGSLLPFPFGCTVTRTALACYADLLNPPRKAIVALAHAASEPSEARLK 420
QY 782 ALLE---KOAYKEQVLAKRLTMLELEKYPACEMKPFSEFI-ALLPSIRPRYSISSPRV 837
DB 421 FLSSPGKDEYSKWVGSORSLEVMADFPKAPLGVFFAAIAPRLQPRYSISSPRP 480
QY 838 DEKQASITVSVSGEAWSGYKGIASNYLAEL----QEGDTITCFITPQSEFTLPKD 893
DB 481 APQRVHTCALVEGPTPTG-RIHKGVCSTWMSKATPLEKSHDCSRAPIFIRPSNEKLPAD 539
QY 894 PETPLMVGGTGVGAPFGFVGVOARKOLKEQOSLGEAHLYFCGRSPHEDYLYQEELENAQ 953
DB 540 HSIPILMVGGTGVGFLGFLQRLAKEDGVQLGALLFFGCRNRQMDFIYEDELNNFV 599
QY 954 SEGIIIT-LHTAFSRPNQPKTYVQHVMEQDGKKLIELLDQGAHFYTCGDSQMAPAVEAT 1012
DB 600 QQGAISELIVAFSR-EGPEKEYVQHKKMDKAEVLSLSIQGGYLYVCGDAKGMARDVHRS 658
QY 1013 LMKSYADVHQVSEAD---ARLWQOLEEKRYAKDVW 1046
DB 659 L---HTIVQQEENADSSKAEATVKKLQMDGRYLDRDW 692
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Search completed: May 29, 2003, 08:31:43
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:51 ; Search time 26 Seconds
(without alignments)
1671.815 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIREMPQKPTFGELKNPL.....RLWLOLEKGRYAKDWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5457	100.0	1048	1	CPXB_BACME
2	3314	60.7	1061	1	CYPD_BACSU
3	3281.5	60.1	1054	1	CYPE_BACSU
4	778.5	14.3	677	1	NCPR_MOUSE
5	777.5	14.2	677	1	NCPR_RAT
6	769	14.1	677	1	NCPR_PIG
7	769	14.1	679	1	NCPR_RABIT
8	767	14.1	676	1	NCPR_HUMAN
9	761.5	14.0	677	1	NCPR_CAVPO
10	735.5	13.5	671	1	NCPR_MUSDO
11	725.5	13.3	679	1	NCPR_DROME
12	723	13.2	601	1	NCPR_SALTR
13	721	13.2	690	1	NCPR_PHAU
14	702	12.9	714	1	NCPR_CATRO
15	679.5	12.5	1147	1	NOS2_RAT
16	679	12.4	1429	1	NOS1_MOUSE
17	678	12.4	1429	1	NOS1_RAT
18	675	12.4	1434	1	NOS1_HUMAN
19	671.5	12.3	1147	1	NS2D_HUMAN
20	665.5	12.2	1144	1	NOS2_MOUSE
21	662	12.1	1435	1	NOS1_RABIT
22	661	12.1	1153	1	NS2A_HUMAN
23	655	12.0	1136	1	NOS2_CHICK
24	651.5	11.9	1149	1	NOS2_CAVPO
25	642	11.8	1174	1	NOS2_RHOPR
26	639	11.7	680	1	NCPR_CANNA
27	634.5	11.3	1247	1	NOS_ANOST
28	608.5	11.2	1202	1	NOS3_HUMAN
29	602.5	11.0	1204	1	NOS3_BOVIN
30	594.5	10.9	1201	1	NOS3_MOUSE
31	590.5	10.8	1204	1	NOS3_PIG
32	587	10.8	680	1	NCPR_CANTR
33	564.5	10.3	1350	1	NOS_DRAME

34	563	10.3	496	1	NOS2_RABIT
35	537.5	9.8	678	1	NCPR_SCHPO
36	534.5	9.8	725	1	MTRR_HUMAN
37	522	9.6	690	1	NCPR_YEAST
38	518.5	9.5	598	1	CYSJ_ECOLI
39	500.5	9.2	1153	1	NOS_DYMS
40	495.5	9.1	598	1	CYSJ_SALTY
41	488.5	9.0	601	1	CYSJ_BUGAI
42	480.5	8.8	919	1	NOS3_RAT
43	466.5	8.5	682	1	MTRR_CABEL
44	460	8.4	576	1	C972_SOYBN
45	459.5	8.4	580	1	C973_ARATH

ALIGNMENTS

RESULT 1
CPXB_BACME
ID CPXB_BACME STANDARD; PRT; 1048 AA.
AC P14779;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450(BM-3))
DE (P450BM-3) [includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-
DE cytochrome P450 reductase (EC 1.6.2.4)].
GN CYP102A1 OR CYP102.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID-1404;
RN [1]
RP MEDLINE-89291834; PubMed-2544578;
RA Ruettiger R.T., Wen L.-P., Fulco A.J.;
RT "Coding nucleotide, 5' regulatory, and deduced amino acid sequences
RT of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450
RT reductase from Bacillus megaterium.";
RL J. Biol. Chem. 264:10987-10995(1989).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE-92088245; PubMed-1727637;
RA Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,
RA Peterson J.A.;
RT "Fatty acid monooxygenation by P450BM-3: product identification and
RT proposed mechanisms for the sequential hydroxylation reactions.";
RL Arch. Biochem. Biophys. 292:20-28(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.
RX MEDLINE-93342510; PubMed-8342039;
RA Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,
RA Deisenhofer J.;
RT "Crystal structure of hemoprotein domain of P450BM-3, a prototype for
RT microsomal P450 S.";
RL Science 261:731-736(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.
RX MEDLINE-97185914; PubMed-9033595;
RA Li H.Y., Poulos T.L.;
RT "The structure of the cytochrome P450BM-3 haem domain complexed with
RT the fatty acid substrate, palmitoleic acid.";
RL Nat. Struct. Biol. 4:140-146(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 459-649.
RX MEDLINE-99162523; PubMed-10051560;
RA Sevriloukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;
RT "Structure of a cytochrome P450-redox partner electron-transfer
RT complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:18663-18668(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.
RX MEDLINE-21552922; PubMed-11695892;
RA Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;

RT "Pivotal role of water in the mechanism of P450BM-3.";
 RL Biochemistry 40:13456-13465(2001).
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES
 CC HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,
 CC OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16
 CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
 CC P450.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferrocyclochrome.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
 CC P450 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL: J04832; AA87602.1; -
 CC PIR: A34286; A34286.
 CC DR PDB: 2HPD; 31-OCT-93.
 CC DR PDB: 2BMH; 31-JUL-94.
 CC DR PDB: 1FAG; 12-FEB-97.
 CC DR PDB: 1FAH; 12-FEB-97.
 CC DR PDB: 1B07; 23-SEP-98.
 CC DR PDB: 1BVY; 23-FEB-99.
 CC DR PDB: 1JPZ; 09-NOV-01.
 CC DR InterPro: IPR001128; Cytochrome_P450.
 CC DR InterPro: IPR003097; FAD_binding.
 CC DR InterPro: IPR001709; FPN_cyt_redtase.
 CC DR InterPro: IPR001226; Flavodoxin.
 CC DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 CC DR Pfam: PF00067; p450; 1.
 CC DR Pfam: PF00175; NAD_binding; 1.
 CC DR Pfam: PF00258; flavodoxin; 1.
 CC DR Pfam: PF00667; FAD_binding; 1.
 CC DR PRINTS; PR00371; FPNCR.
 CC DR PRINTS; PR00385; P450.
 CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 CC KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 CC KW Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.
 CC FT INIT_MET 0 0
 CC FT DOMAIN 1 471 CYTOCHROME P450.
 CC FT DOMAIN 472 1048 NADPH-P-450 REDUCTASE.
 CC FT BINDING 400 400 HEME.
 CC FT TURN 12 13
 CC FT TURN 15 16
 CC FT TURN 17 20
 CC FT HELIX 25 36
 CC FT STRAND 39 44
 CC FT TURN 45 46
 CC FT STRAND 47 52
 CC FT TURN 55 61
 CC FT HELIX 62 62
 CC FT TURN 64 66
 CC FT STRAND 67 69
 CC FT HELIX 73 82
 CC FT TURN 83 84
 CC FT HELIX 86 88
 CC FT TURN 91 92
 CC FT HELIX 94 107
 CC FT TURN 109 111
 CC FT HELIX 112 131
 CC FT TURN 132 132
 CC FT TURN 135 136
 CC FT TURN 139 140
 CC FT STRAND 141 158
 CC FT HELIX

164 166
 172 189
 197 197
 226 226
 233 238
 239 239
 241 241
 243 245
 248 248
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 Best Local Similarity 100.0%; Pred. No: 9e-298;
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 DB 1 TIKEMPPQKTFGELKNLPLLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
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 DB 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQAMKGYEAMV 120
 QY 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRFNSFYRDQPHPTTSMVRA 180
 DB 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRFNSFYRDQPHPTTSMVRA 180
 QY 181 LDEAMNKLQANRPPDPAYDENKRFQEDIKVNMNDLVDKIIADRKASGEQSDLLTHMLNG 240
 DB 181 LDEAMNKLQANRPPDPAYDENKRFQEDIKVNMNDLVDKIIADRKASGEQSDLLTHMLNG 240
 QY 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLVD 300
 DB 241 KDPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLVD 300
 QY 301 PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLPOL 360
 DB 301 PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGEYPLEKGDMLVLPOL 360
 QY 361 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH 420
 DB 361 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFNGQQRACIGQQFALHEATLVLGMLKH 420
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 DB 421 FDFEDHTNYELDIKETLTLLKPEGVFVVKAKSKIPGLGIPSPSTEQSAKVKRKAENAHNT 480

Db 421 DFEHHTNYELDKETITLTKPEGVVAKSKKIPLGIPSPSTEQSAKKYKKKAENAHNT 480
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 Db 481 PLVLVYSGNMGTAEGTARDLADLAMSQFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540
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 Db 541 PDNAKQVWLDQASADEVKGVRYSVFGCGDKNWTYYQKVPAFIDETLAAGAENIADR 600
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 QY 901 VGPCTGVAPRGFVQARKQKLEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960
 Db 901 VGPCTGVAPRGFVQARKQKLEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960
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 Db 961 HTAFSRMPNPKTVVQVHMVQDQKLLLELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
 QY 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048
 Db 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048

RESULT 2

ID CYPD_BACSU STANDARD; PRT; 1061 AA.
 AC O08394;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable bifunctional P-450:NADPH-P450 reductase 1 [includes:
 DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
 DE (EC 1.6.2.4)].
 GN CYPD OR CYP102A2.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=97453479; PubMed=9308178;
 RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
 RA Duesterhoeft A., Ehrlich S.D.;
 RT "Sequence of the Bacillus subtilis genome region in the vicinity of
 RT the lev operon reveals two new extracytoplasmic function RNA
 RT polymerase sigma factors SigV and SigZ.";
 RL Microbiology 143:2939-2943(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., S.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell J.F., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conner I.B., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara B., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche M., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenberg M., Vannier P., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
 RA Winters P., Wipac A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
 CC P450 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferrocyclochrome.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
 CC P450 FAMILY.
 CC -----
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 CC -----
 CC EMBL; D87979; BAA20123.1; -;
 DR EMBL; Z99107; CAB12544.1; -;
 DR HSSP; P14779; 1JFZ.
 DR Subtilist; BG12871; cypd.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00067; p450; 1.
 DR Pfam; PF00175; NAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00667; FAD_binding; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
 KW Complete proteome.
 FT DOMAIN 1 474 CYTOCHROME P450.
 FT BINDING 475 1061 NADPH-P-450 REDUCTASE.
 FT BINDING 403 403 HEME (BY SIMILARITY).
 SQ SEQUENCE 1061 AA; 119467 MW; 7915DACC20578978 CRC64;
 Query Match 60.7%; Score 3314; DB 1; Length 1061;

Best Local Similarity 59.5%; Pred. No. 7.1e-178;

Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 SRFDKNLQALKFVRDFAGDGLFTSWTHEKNMKKAHNLPSFSQAKGYHAMVDIAV 124
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 ERFDKSTEGALVRAFSGDLFTSWTHEPNRKAHNLMPFESQAKMDYHEKWDIAV 126
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QY 125 QLVQKWERLNADHIEVPEDMTLTLDTGLCGFNFRFNSFYDQPHPTTSVWRALDEA 184
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QY 127 QLIQKWARLNPNADVDPGDMTTLTLDTGLCGFNFRFNSFYDQPHPTTSVWRALDEA 186
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QY 304 SYQVQKLVYGVMLNEALRLWPTAPAFSLYAKEDVILGGEYPLEKGDMLVLIPLHRD 363
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QY 367 RDWAGKDAEFREREHQDQVPHAYKFPNGORACIGQFALHEATLVGLMGLKHEDF 426
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 427 IDHNTYELDKETLTKPEGVVKAQSKXIPILGGIPSPTEQSA---KKVRKAENA--- 486
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 487 GLNRPFLVLYGSDTGTAGVARELADTASLGRVTKTAPLNDRIKLRKPGAVLVTSS 546
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 YNGHPDPAQFQVWLDQASADSVKGVRSYVFCGDKNWTATYQKVPFIDETLAAGAE 595
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 547 YNGKPPSNAGQFQVWLDQASADSVKGVRSYVFCGDKNWTATYQKVPFIDETLAAGAE 606
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 607 RFSARGEDVSGDFQELDEKSMWADAIAKAFGLNELNADKERSTLSLQFVGLGESP 666
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 655 LAKMHGAFSTNVVAKELQPGSARSTRHLEIPLKREASYQEGDHLGVIPRNYEGVNV 714
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 787 PPHRELELSAEGVYQEQILKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRI 846
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 1026 QKAYQAVHGTGEQEAQNWLRLHLDQTMGYAKDVWAG 1060
RESULT 3
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AC O08336;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)]
GN CYTE OR CYP102A3.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Dusterhoeft A., Ehrlich S.D.;
RA "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors SigV and SigZ."
RL Microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Chouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Crouillet S., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denisot F., Devine K.M., Dusterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
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RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogawa A., Oudega B., Park S.H.,
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RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosoato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
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 DR EMBL; U93874; AAB80867.1; -;
 DR EMBL; Z99117; CAB14658.1; -;
 DR HSSP; P14779; LJPZ.
 DR Subtilist; BG12299; cYPE.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00067; P450; 1.
 DR Pfam; PF00175; NAD_binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00667; FAD_binding; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
 KW Complete proteome.
 FT DOMAIN 1 475 CYTOCHROME P450.
 FT BINDING 472 1053 NADPH-P-450 REDUCTASE.
 FT BINDING 403 403 HEME (BY SIMILARITY).
 SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866CAL10 CRC64;

Query Match 60.1%; Score 3281.5; DB 1; Length 1054;
 Best Local Similarity 58.5%; Pred. No. 4.6e-176;
 Matches 614; Conservative 173; Mismatches 254; Indels 9; Gaps 6;

QY 5 MPQPKTGGELKNLPLNTDKPVQALMKIADBLGIFKEAPGRVTRLYSLSORLKEACDE 64
 Db 7 IPQPKTYGPLNPLEHLEKEQLSLSLWRIADLGLGIFRDFPGVSVFVSGHNLVAECDE 66
 QY 65 SRFDKNLSOALKFYRDFAGDGLFTSWTHKNNKKAHLLPFSQQAQMGVHAMVVDIAV 124
 Db 67 KRFDKNLGKLGKQVREFGDGLFTSWTHKNNKKAHLLPFSQQAQMGVHAMVVDIAV 126
 QY 125 QLVQKWERLNADERIEVPEDTRTLDTIGLCGFNYRFSFYRDPHPFITSVMRALDEA 184
 Db 127 QLVQKWERLNADERIEVPEDTRTLDTIGLCGFNYRFSFYRDPHPFITSVMRALDEA 186
 QY 185 MNKLQANPDPAVDENKRFQEDIKVNDLVKIIADRKASGEQS-DLLTHMLNGKDP 243
 Db 187 MNQSKRLGLQDKMVKTKLQFQKDIEVMSLVDRMIAERKANPDENIKDLSLSLYAKDP 246
 QY 244 ETGEPDLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAARVLPVP 303
 Db 247 VTGETLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAARVLPVP 306
 QY 304 SYQVQKVLKYGVMNEALRLWTPAPAFSLYAKEDTVLGGFPLEKQDELMLVLPQLHRD 363
 Db 307 EYKQIQQLKYRMVNLRLPYTPAPAFSLYAKEDTVLGGFPLEKQDELMLVLPQLHRD 366
 QY 364 KTINGDDVEERPRPFENPSAIPQAHKPFNGQACIQGFALHEATVLMGLMKHFD 423
 Db 367 QNAGWDPAEDPRPFEDPSSIPHHAYKPFNGQACIQGFALHEATVLMGLMKHFD 426
 QY 424 EDHFNIEDIKETITLKEGFPVVKAKSKKIPGLGIPSPSTBQS---AKVKKKAENAHNT 480
 Db 427 INHGYELKIEALTIKPDPIKTVKPRK--TAAINVQRKEQADIKATKPKPKPHGT 484
 QY 481 PLLVLYSGNMGTAEGTARDLADIAMSKGFAPOVATLDSHAGNLPREGAVLITVASYNGHP 540
 Db 485 PLLVLYSGNLTAEIAGELAAQGRMGFTETAPLDDYIGKLPREGAVLITVASYNGAP 544
 QY 541 PDNAKQFVDWLDQASADEVKGVRSVFEGCGDKNNWATTYQKVPAPFIDETLAAGAENIADR 600

Db 545 PDNAGFVFWLKEEGOLKGVSAVFCGNGRWSASTYQIRPLTDDNMKAGASRLTAI 604
 QY 601 GEADASDDFCTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMLAKMHG 660
 Db 605 GEGDAADDFFESHRESNENRFWKTDAPDIMEIAQKDRPSLITFLSEATETPVAKAYG 664
 QY 661 AFSTNVVASKLOQFGSARSSTRHLEIPLKEASTQEGDHLGVIPRNYEGIVNRYTAREGL 720
 Db 665 AFEGLVLENRELQATASTRSTRHLEIPLKEASTQEGDHLGVIPRNYEGIVNRYTAREGL 724
 QY 721 DASQIRLEAEEKLAHLPLAKTVSVEELL-QYVELQDPVTRTORLMAAATVCPHPHVE 779
 Db 725 QSNHVIKVSAGAH-MAHLPMDRPIKVVDLLSSYVELQEPASRLQRLRELASTVCPHPOKE 783
 QY 780 LEALLEKQA-YKEQVLAKRLTLELEKYKACEMKFSFEIALLSIRPRYSISSSPVD 838
 Db 784 LEQLVSDGIIYKEQVLAKRLTLELEKYKACEMKFSFEIALLSIRPRYSISSSPVD 843
 QY 839 EKQASITVSVVSGEAWSGYGEYKGTASNYLAELQEGDTITCFSTPQSEFTLPKDPETPL 898
 Db 844 ANIVSMIVGVVKSASWSGRGEYGVASNYLAELTGDAAACFIRTPQSGFQMPNDPPTM 903
 QY 899 IMVPGTGVAPFRGFVQARKOLKEGOSLGEAHLYFGCRSPHEDYLYOELENAQSEGI 958
 Db 904 IMVPGTGVAPFRGFVQARKOLKEGOSLGEAHLYFGCRSPHEDYLYOELENAQSEGI 963
 QY 959 TLHTAFSRPNQPTVQVHMEQDKKLIELLDGAFYICGDSQSOMAPAVEATLMSKYA 1018
 Db 964 TIRRCYSRVNEPKGYVQHLKQDTQKLTUETKGAHIYVCGDSQSOMAPADVERTLRLAYE 1023
 QY 1019 DVHGVSEADARLWQLEEKGRYARDVWAG 1048
 Db 1024 AEKASQESAVWLKQDQRRYKDVWG 1053
 RESULT 4
 NCPR_MOUSE
 ID NCPR_MOUSE STANDARD; PRT; 677 AA.
 AC P37040;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN POR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ddy;
 RX MEDLINE=94281246; PubMed=8011664;
 RA Ohgaya S., Ishizaki K., Kamataki T., Shinriki N.;
 RT "Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and functional expression in yeast."
 RL Biochim. Biophys. Acta 1186:137-141(1994).
 CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2 ferrocycytochrome.
 CC -!- COFACTOR: FAD AND FMN.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
 CC -----
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DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00667; FAD_binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane; Acetylation.
 FT MOD_RES 72 72 ACETYLATION.
 FT NP_BIND 171 202 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 315 326 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 452 462 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 530 548 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 625 641 NADP (ADP PART) (BY SIMILARITY).
 FT CONFLICT 40 41 YW -> NY (IN REF. 2).
 FT CONFLICT 53 53 E -> N (IN REF. 2).
 SQ SEQUENCE 679 AA; B1A163FA53A5988B CRC64;
 Query Match 14.1%; Score 769; DB 1; Length 679;
 Best Local Similarity 31.7%; Pred. No. 8.9e-36;
 Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;
 QY 444 FVYKAKSKIP-----LGIPSPSTEQA--KVKRKAENAHTPLLYLGSNMGTAEGTA 497
 DB 42 FLFRKKKEVPETKIQAPTSVSSVKESSEFVEKMKKTGRN-----IVFYGSQTGAEEFA 96
 QY 498 RLADIAMSGFAPQVATLDH-----AGNLPREGAVLIV--TASY-NGHPDPNKAQFVOW 550
 DB 97 NRLSKDAHRYGMRGMAADPEYDLADLSLPEINNALAVFCMATYGGEDPTDNAQDFYD 156
 QY 551 LDAQADEVGVSYVFGCGDKNWTYQKVA---FIDETLAAGAENATADGEADSD 607
 DB 157 LQETDVD--LSGVAVFGLNK-----TYEHFNAMGKYVDQRLQGLGQRIFFELGMGDDA 211
 QY 608 DFEGTYEWEHMSVDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPAKMH----- 659
 DB 212 NLEEDFTWREQFWPACVCFHVEATGEESIRQYELVL---HTDIDVAKVYQGMGRK 268
 QY 660 -----GAFSTNVASVELQOPGASRSTRHLEIEL-PKEASYQSGDHLGVIPRN 706
 DB 269 SYENQKPPDAKPFATVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVPAN 327
 QY 707 YEGIVNRTARFGLDASQOI---RLEAEKEKLAHPL-----AKTVSV 746
 DB 328 DSALVNLGELTGADLDVMSLNNLDESNKHPFCPTSYRTALTYILDTNPPRNVL 387
 QY 747 EELQVVELQDPVTRTOLRAMAKTVCPHPHVEALEALEKQAYKEQVLAKLRLMLELEK 806
 DB 388 YELAQA--ADPAEQQLRKMASSG-----EGKELYLSWVVEARRHILAILQD 434
 QY 807 YPACEMKFSEFIALLPIRPIRYYSISSPRVDEKQASITVSVSGEAWSGYGEYKGTASN 866
 DB 435 YPSLRPPIDHLCLELLPRLQARYYSIASSSKVPNSVHICAVAVEYETKAGRLN-KGVATS 493
 QY 867 YL-AELQEGDT-----ITCFISYQSEFTLPKDPETPLIMVPGCTGVAPRFGFQARKQL 920
 DB 494 WLRAKEPAGNGRGLVPMFVR--KSQRLPFFKATTPVIMVPGCTGVAPRFGFQARKQL 551
 QY 921 KEQGSGLAEHLFGCSHEDYLYQEELENAQSEGIIT-LHTAFSPNPNQKTYQGVHM 979
 DB 552 RQQGEVGETLLYGCRRAAEDYLYRELAGFKDGLTSLQNLVAFSEQAQ-KVYVQHLL 610
 QY 980 EQDGKLIELLDQ-GAHFYTCGGSGQMAPAVETATLMKSYADVHQVSPADARLMQLQLEEK 1038
 DB 611 RRDKEHLWRLTHEGGAHIYVCGDARNARDVQNTFYDIVAELGAHQAQVYVVKLMTK 670
 QY 1039 GRVAKDYWA 1047
 DB 671 GRVSLDWS 679

RESULT 8

NCPR_HUMAN

ID NCPR_HUMAN STANDARD; PRT; 676 AA.

AC P16435; Q16455; Q9H3M8;

DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN POR OR CIPOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90105390; PubMed=2513880;
 RA Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;
 RT "Structural and functional analysis of NADPH-cytochrome P-450
 RT reductase from human liver: complete sequence of human enzyme and
 RL NADPH-binding sites";
 RL Biochemistry 28:8639-8645(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92198003; PubMed=1550342;
 RA Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
 RT "Quantification of cytochrome P450 reductase gene expression in human
 RT tissues";
 RL Arch. Biochem. Biophys. 294:168-172(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Czerwinski M., Sahni M., Madan A., Parkinson A.;
 RT "Polymorphism of human CYPOR: expression of new allele";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Murakami H.O., Ogawa H., Nisimoto Y.;
 RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase
 RT in human HL-60 cell";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.
 RX MEDLINE=99156068; PubMed=10048323;
 RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
 RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;
 RT "Crystal structure of the FMN-binding domain of human cytochrome P450
 RT reductase at 1.93 A resolution";
 RL Protein Sci. 8:298-306(1999).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
 CC ferrocycytochrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 CC -----
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 CC -----
 CC EMBL; S90469; AAB21814.1;
 DR EMBL; AF258341; AAG09798.1;
 DR EMBL; AB051763; BAB18572.1;
 DR PIR; A33421; A33421.
 DR PDB; 1B1C; 24-NOV-99.
 DR Genew; HGNC:9208; POR.
 DR MIM; 124015; -

Db 385 ELAEY--CSEKDEKFLRNMASTIT---PE-----GREKYQWJQNSRNVHLEDI 431
QY 808 PACEMKFSEPIALLPSIRPRYSISSPRVDEKQASTVSVSSEAWSGVGEYKGTASNY 867
Db 432 KSCRPIIDICELPLRPRIYISSSSKLYPTNVHITAVTVOYETPTGRVN-KGVATSY 490
QY 868 LAELOE--GDT-ITCFISTPQSEFTLPKDPETPLIMVGPOTGVAPFRGFQAKOLKEQG 924
Db 491 MKEKNPSVGEVKVPVEIR--KSQFRLPTKSEIPIIMVGPCTGLAPFRGFIQRQLRDG 548
QY 925 QSLGEAHLFGCRSPHEDYLYQBELENAQSEGLITHTAFSPMPNQPKYVQVHMVQDCK 984
Db 549 KVVGDITLYFGCRKDEDEFTYRELEQYVQNGFTLTAKFSR--DOQEKIYVTHLIEQDAD 607
QY 985 KLELL--DOGAHYICGDSQMAVEATLMSYADVHOVSEADRLWLQOLEEKRYAK 1043
Db 608 LIKWVIGEGKHGFIYCGDAKNMAYDVNLYLKILSTYKGNMNSDAVQYIKKMEARISA 667
QY 1044 DWNA 1047
Db 668 DVNS 671

RESULT 11

NCPR_DROME STANDARD; PRT; 679 AA.
AC Q27597; Q9VMF2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN CPR OR Cg11567.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7221;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=Canton-S; TISSUE=Antenna;
RX MEDLINE=97311413; PubMed=9168130;
RA Hovenann B.T., Sehlmeier F., Malz J.;
RT "Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:
RT pronounced expression in antennae may be related to odorant
RL Gene 189:213-219(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.D.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou X., Zhou L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5. MAY FUNCTION TO
CC CLEAR THE OLFACTORY ORGAN (ANTENNAE) FROM ACCUMULATING CHEMICALS.
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocycytochrome.
CC -!- COFACTOR: FAD AND FMN.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGH IN ANTENNAE.
CC -!- DEVELOPMENTAL STAGE: EMBRYOS AND ADULTS.
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADPH+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X91090; CAA63639.1; -
CC EMBL: A5003613; AAF52367.1; -
CC HSP: P16435; IBIIC.
CC Flybase: FBgn0015623; Cpr.
CC InterPro: IPR003097; FAD_binding.
CC InterPro: IPR001709; FPN_cyt_reductse.
CC InterPro: IPR001094; Flavodoxin_like.
CC InterPro: IPR001226; Flavodoxin.
CC InterPro: IPR001433; Oxred_FAD/NAD(P).
CC Pfam: PF00175; NAD_binding; 1.
CC Pfam: PF00258; flavodoxin; 1.
CC Pfam: PF00667; FAD_binding; 1.
CC PRINTS: PR00369; FLAVODOXIN.
CC PRINTS: PR00371; FPNCR.
CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
CC Membrane.
KW NP_BIND 176 207 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 320 331 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 457 467 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 537 555 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 632 648 NADP (ADP PART) (BY SIMILARITY).
FT CONFLICT 38 39 AA -> VT (IN REF. 1).
FT CONFLICT 45 45 S -> T (IN REF. 1).
FT CONFLICT 132 132 I -> T (IN REF. 1).
SQ SEQUENCE 679 AA; 76346 MW; C6387C11A0EDB4A CRC64;

Query Match 13.3%; Score 725.5; DB 1; Length 679;
Best Local Similarity 29.8%; Pred. No. 2.4e-33;
Matches 191; Conservative 113; Mismatches 257; Indels 79; Gaps 21;
QY 460 SPSTEQSAKKYKKAENAHNTPLLVLYGNSMCTAGSTARDLADIAAMS---KGFA--POVA 514
Db 67 SASDNSFIKKLA-----ASGRSLVVFYGSQTGTGEEFAGRLAKEGIRYKLGWADPEEC 121

Qy 515 TLDS--HAGNLPREGAVLIIVTASNGHPDPAKOFVWLDQASADEKGVYRYSVFGCGDK 572
 Db 122 DMEELLQKIDNSLAVFCLATYCEGDPDNAMEFYEMITSGVDV-LSGLNYAVFGLGNK 180
 Qy 573 NWATTYQKVPFIDETLAAGAENIADRGADSDDEGEEYEEVREHMSDVAAYFNLDI 632
 Db 181 TY-EHYNKVAIYVDKREELGAGNRFELGLGDDDDANIEDFITWKDRFWPACVDFHG--I 237
 Qy 633 ENSDNKSTLSQVDSAADMP-----LAKMH-----GAFSTNVVASKELQ 673
 Db 238 EGGEEVLIROYRLLEQDPVDPDRIYTGERTARLHSIQNRPDPFPAKPFILAPIKNRELH 297
 Qy 674 QPSGARSTRHLEIPL-KEASYQEGDHLGVIPRNYEGIVNRVTRARFGLDAS--QQIRLE 729
 Db 298 K-GGGRSCMHIELSIEGSKMRYDAGDHVAMPFVNDKSLVEKLGQLCNADLDTVFSLINTD 356
 Qy 730 ABEKLAHL-----LAKTVSVEELQVYELQDPVTRTQLRMAAKTV 772
 Db 357 TDSKKHFPFPPPTTYRTALTHTYLEITAPRTHILKLAEY--CTDEKEKELLRSMA--SI 412
 Qy 773 CPPHKVEALLEKQAYKEOVLAKRLTMELEKYPACEMKFSFIALPSIRPRYSIS 832
 Db 413 SPE-----GREKQSWIQDACRNVHILEDIKSCRPIDHVCCELLPRQPRYSIS 463
 Qy 833 SSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYLAELQ-----EGDTITCFISTPOSEF 888
 Db 464 SSALKHPTDHTVAVLVEYKTPTRIN-KGVATTYLNKQPOGSEEVKVPVFI--KSQF 520
 Qy 889 TLPKDPETPLMWPGTCVAFPGFVQARQKQKQSGSLGHAHLYFCGRSPHEDYLQEE 948
 Db 521 RLPTPTPIIMVPGTGLAPFGRFIOERQFLRDEGTVGESILYFCGRKRSEDIYIESE 580
 Qy 949 LENAQSGEITLHTAFSRMPNPKTYVOHVMEQDGKLIELLDG-AHFYICGDSQMAP 1007
 Db 581 LEWVKGTNLNKAAPSRDQCK-KVYVQHLLLEQDADLIWNVIGENKGFHYICGDAKNVAV 639
 Qy 1008 AVEATLMKSVADHVQVSEADARLWQLEEKGRYAKDWA 1047
 Db 640 DVNRILKILSTKGMSEADAVQYIKKMEAKRYSADVWS 679

RESULT 12

NCPR_SALT
 ID NCPR_SALT STANDARD; PRT; 601 AA.
 AC P19618;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
 DE (Fragments).
 OS Salmo trutta (Brown trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8032;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88008061; PubMed=3116019;
 RA Urenjak J., Linder D., Lumper L.;
 RT "Structural comparison between the trout and mammalian hydrophilic
 domain of NADPH-cytochrome P-450 reductase.";
 RL J. Chromatogr. A 397:123-136(1987).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 TO CYTOCHROME P450 IN MICROSOSES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferriocytocrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 DR PIR: A28577; A28577.
 DR HSP; P16435; IBIIC
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR PRINTS; PR00369; Flavodoxin.
 DR PRINTS; PR00371; FPNCR.
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane.
 FT NON_TER 1 1
 FT NON_CONS 426 427
 FT NON_CONS 434 435
 SQ SEQUENCE 601 AA; 68304 MW; BC801767DELD44C9 CRC64;
 Query Match 13.28; Score 723; DB 1; Length 601;
 Best Local Similarity 30.2%; Pred. No. 2.8e-33;
 Matches 195; Conservative 106; Mismatches 239; Indels 106; Gaps 21;
 Qy 459 PSPTEQSA--KKVRKKAENAHNTPLLVLYGNSNMGTAEGTARDLADIAMSKGFAPQVATL 516
 Db 5 PAPSTQETSFEKKMKTKGRN-----IVFYGSQTGTGEFANRLSKDAHRYGMSGMAADP 59
 Qy 517 D-----SHAGNLPREGAVLIIV--TASY-NGHPDPAKOFVWLDQASADEKGVYRYSVFGC 569
 Db 60 EYDMSELRLAEIGNSLAIFCMATYGECDPTDQADFYDWL-QETDGLQSLGVNYPVFEAL 118
 Qy 570 GDKNWTYQKVPFIDETLAAGAENIADRGADSDDEGEEYEEVREHMSDVAAYFN 629
 Db 119 GDKTY-EHYNKVAIYVDKREELGAGNRFELGLGDDDDANIEDFITWKDRFWPACVDFHG 177
 Qy 630 LDIENSNDKSTLSQVDSAADMPAKMH-----GAFSTNVVAS 669
 Db 178 VEASGEDSSVROVELK-----EHDNMKNVYTGELGRKLSFETQKPPDKNPFAPVTN 234
 Qy 670 KLOQPCASSTRHLEIPL-KEASYQEGDHLGVIPRNYEGIVNRVTRARFGLDASQIRL 728
 Db 235 RKLKAGELHK-MHELVDTGSKTRYESGDHVAVYPTNNTVIVNRGLQILGVLDLDSVLSL 293
 Qy 729 EAEEEK-----LAHLPLAKTVSVBELQY-VELODPVTRTOLR 765
 Db 294 NNLDESNKKHPPFPCPTTYRTALTHTYLDIHP--RTNVLXELAQYATDLKQENTDSMA 351
 Qy 766 AMAAKTVCPHPKVEALEKQAYKEOVLAKRLTMELEKYPACEMKFSFIALPSIR 825
 Db 352 SSAPE-----GKALYQSFVLENNRNLAILLEDLPRLRPIDHLCMLPRLQ 397
 Qy 826 PRYSISSSPRVDEKQASITVSVSGEAWSGYGEY--KGIASNYLAELQEGDTITCFIST 883
 Db 398 ARYYSIASSSKVPNSHICAVLV-----EYTKGVATTWLKYLIR----- 437
 Qy 884 POSEFTLPKDPETPLMWPGTCVAFPGFVQARQKQKQSGSLGHAHLYFCGRSPHEDY 943
 Db 438 -KSQFRLPFRASNPVIMVPGTGIAPMGFIQERGLWKEKSGKEVGETVLYCGCRKKEEDY 496
 Qy 944 LYQEELENAQSGEIT-LHTAFSRMPNPKTYVOHVMEQDGKLI-IELDQAHFYTCGD 1001
 Db 497 LYQEELENAQKKGALTKLNVAFSREDOQ-KVYVQHLLRKNKVDLWRQIHEDYAHYICGD 555
 Qy 1002 GSNAPAVEATLMKSVADHVQVSEADARLWQLEEKGRYAKDWA 1047
 Db 556 ARNARDVQTAFYETAEELGGMTRTQATDYIKKLTGKRYSDVWS 601

RESULT 13

NCPR_PHAU
 ID NCPR_PHAU STANDARD; PRT; 690 AA.
 AC P37116;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 OS Phaseolus aureus (Mung bean) (Vigna radiata).

Db	251	TPYTAALRYRVVIHPTAASTYDNHSTVANGNTEFDIIHPCRVNAVQKELHKPESDRS	310
QY	681	TRLETELP-KEASYGEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEKLAHL-	738
Db	311	CIHLEFDISGTSITYDTGDHVGVAENCTVETGKLLQNLDLFLSLTKDGDGTSIG	370
QY	739	-----PLAKTVSYE-ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---	KQAY 789
Db	371	GSLPPFPFGCSLRTALARYADLLNPPRKAALLALATH-ASEPSDERLKFSLSSPQGDKEY	429
QY	790	KEOVLAKRLTMLLELKEYPACEMKFSEFI-ALLPSINPRYISISSPRVDEKQASITVS	848
Db	430	SKVWGSQSLVEMVAEFPSSAKPPLGVFFFAAIPRLQPRYISISSPRFAPQVRHVTCAL	489
QY	849	VSGEAMSGYGEYKGIASNYL-----AEIQEGDTITCFISTPOSEFTLPKDPETPLIMVG	902
Db	490	YVGTPFG-RIHKGVCSTWKNNAIPEKSDQCSAPFIR--PSNFKLPVDHSIPLIMVG	546
QY	903	PGTGVAFFRGFVOARKQLKEQGOSGLGEAHLFYGCRSPHEDYLYQEELENAQSEGIIT-LH	961
Db	547	PGTGLAPFRGLQERYALKEDGVOLGALLFFGCRNRQMDFIYEDELKSFVEQGSISELI	606
QY	962	TAFSRMNPQKTVYQHVMEQDGKLLLELDQGAHFHYICGDSQMAFAVEATLMKSTADVH	1021
Db	607	VAFSR-EGAEKEYVQHKMDKAAHLSLSQGGYLYVCGDAGKWARDVHRTLSHIVQEQE	665
QY	1022	QVSEADARLWLOLEEKGRYAKDVW	1046
Db	666	NVDSTRAEALVKKLQMDGRYLRDVW	690

RESULT 14

ID	NCPR_CATRO	STANDARD;	PRT;	714 AA.
AC	Q05001;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).			
GN	CPR.			
OS	Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;			
OC	Vinaceae; Catharanthus.			
OX	NCBI_TaxID=4058;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=94035173; PubMed=8220474;			
RA	Meijer A.H., Lopes Cardoso M.I., Voskuilen J.T., de Waal A.,			
RA	Verpoorte R., Hoge J.H.C.;			
RT	"Isolation and characterization of a cDNA clone from Catharanthus			
RT	roseus encoding NADPH:cytochrome P-450 reductase, an enzyme essential			
RT	for reactions catalysed by cytochrome P-450 mono-oxygenases in			
RT	plants";			
RL	Plant J. 4:47-60(1993).			
RN	[2]			
RN	SEQUENCE OF 1-11 FROM N.A.			
RC	SPRAIN-cv. Morning mist;			
RC	Lopes Cardoso M.T., Meijer A.H., Rueb S., Quelroz Machado J.,			
RA	Memelink J., Hoge J.H.C.;			
RA	Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases			
CC	-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP			
CC	TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON			
CC	TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.			
CC	-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2			
CC	ferricytochrome.			
CC	-1- COFACTOR: FAD AND FMN.			
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE			
CC	ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.			
CC	-1- SIMILARITY: THE FAD-BINDING DOMAIN IS RELATED TO BACTERIAL			
CC	FLAVOXOINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN			


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CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC -----
CC EMBL: X69791; CAA49446.1; -
CC DR EMBL: Y09417; CAA70571.1; -
CC DR PIR: S31502; S31502.
CC DR HSSP: P00388; IAMO.
CC DR InterPro: IPR003097; FAD_binding.
CC DR InterPro: IPR001709; FPN_cyt_redctse.
CC DR InterPro: IPR001094; Flavodoxin_like.
CC DR InterPro: IPR001226; Flavodoxin.
CC DR InterPro: IPR001433; Oxred_FAD/NAD(P).
CC DR Pfam: PF00175; NAD_binding; 1.
CC DR Pfam: PF00258; flavodoxin; 1.
CC DR Pfam: PF00667; FAD_binding; 1.
CC DR PRINTS: PR00369; FLAVODOXIN.
CC DR PRINTS: PR00371; FPNCR.
CC DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane.
FT NP_BIND 200 231 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 348 359 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 489 499 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 567 585 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 661 677 NADP (ADP PART) (BY SIMILARITY).
FT NP_BIND 714 714 AA; 78958 MW; DBDD9AF41374CF91 CRC64;
SQ SEQUENCE 714 AA; 78958 MW; DBDD9AF41374CF91 CRC64;

Query Match 12.98; Score 702; DB 1; Length 714;
Best Local Similarity 28.88; Pred. No. 5.4e-374;
Matches 189; Conservative 118; Mismatches 272; Indels 76; Gaps 18;

QY 445 VVAKSKKIPGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSGNMGTAGCTARDLADIA 504
DB 79 VVEPKLIVPKSVVEPEIDEGKK-----FTIFFGQTGTAEFGAKALAEAE 126
QY 505 MSK--GFAQVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDNKQFVMDLQDA 554
DB 127 KARYEKAVIKVIDIDDAADDEEYEFKRETLAFFILATYGDGEPTDNRARFYKWFVEG 186
QY 555 S--ADEVGVKRVYFGCGDKNWTYOKVPAPFIDETLAAKGAENIADRGEDASDDFEGT 612
DB 187 NDRGDWLNKLYGVFGNLGNQY-EHFNKIAKVDEKVAEQGKKRIVPLVLGDDDDQCIEDD 245
QY 613 YEEVREHWSVAAFYNFLDIENSEDNKSTLSLOFV-----DSAADMPLAKMHGAF 662
DB 246 FAARENWPE-----LDNLLRDEDTTSTVTTAAIPEYRVVFPDKSDSLISEANGHA 299
QY 663 S-----TNVVASKELOQPGSARSRIHLELPEKA-SYQBGDHLGVIPR 705
DB 300 NGYANGNTVYDAQHPCRSNVAVRKELHTPASDRSCTHLDFDIAGTGLSYGTGDHVGVCYD 359
QY 706 NYEGVNRVTRARFGLDASQQIRLEAEKLAHL-----PLAKTVSVEELIQVVELQDP 758
DB 360 NLSETVEAEELLNLPETVFSLHADKEDGTPLAGSSLPFPFPCTRTALTRADLLNT 419
QY 759 VTRTOLRAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTLMLELEKYPACEMKFS 815
DB 420 PKKSALLAALAAADPNADRLKYLASPAQKDEYAQSILVANQSRSLLEVMAEFFPSAKPLG 479
QY 816 EFI-ALLPSIPRPRYSISSPRVDEKQASTVSVSGEANSWGYGEYGIASNYLAE---L 871
DB 480 VFFAAIAPRLOPRYSISSSPRMAPSRHVTALVY-EKTPGGRIHKGVCSTWKNKAIPL 538
QY 872 QEG-DTITCTFTSQSEFTLPKDPETPLIMVPGCTGVAPRFGVQARKQLKEQCSQSGEA 930
DB 539 EESRDCSWAPFVQSNFKLPADPKVPVIMIGPCTGLAPRFGFLQERLALKEGAEIGTA 598
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QY 931 HLYFGCRSPHEDYLYQBELENAQSEGILT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIEL 989
DB 599 VFFGCRNRKMDYIYDELNHFLEIGALSELVAFSR-EGPTKQTVQHKMAEKASDIWRM 657
QY 990 LDQGAHFYICGDSQMAPAVEATLMKSVADYVHQVSEADARLWLQQLQLEEKRYAKDVW 1046
DB 658 ISDGAYVYVCGDAKGMDRVHRTLHTIAEQEGSHDSTQAEFVNKLQMTGRYLDRDVW 714

RESULT 15
NOS2_RAT
ID NOS2_RAT STANDARD; PRT; 1147 AA.
AC Q06518; P97774; O35765; Q35766; Q64558; Q64005; Q63267;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS).
GN NOS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle.
RX MEDLINE=93191721; PubMed=7680561;
RA Kunikida Y., Ishida N., Tanaka S.;
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
RL muscle cells.";
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Pancreatic islets;
RX MEDLINE=95309543; PubMed=7540573;
RA Karlens A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
RA Mandrup-Poulsen T., Boel E., Nerup J.;
RT "Cloning and expression of cytokine-inducible nitric oxide synthase
RL cDNA from rat islets of Langerhans.";
RL Diabetes 44:753-758(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Astrocyles;
RX MEDLINE=94231594; PubMed=7513765;
RA Galea E., Reis D.J., Feinstein D.L.;
RT "Cloning and expression of inducible nitric oxide synthase from rat
RL astrocytes.";
RL J. Neurosci. Res. 37:406-414(1994).
RN [4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94039059; PubMed=7693462;
RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,
RA Nagasaki H., Sugimura T., Esumi H.;
RT "Molecular cloning of a cDNA encoding an inducible
RL calmodulin-dependent nitric-oxide synthase from rat liver and its
RL expression in COS 1 cells.";
RL Eur. J. Biochem. 217:37-43(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hepatocytes;
RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RL nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
RX MEDLINE=94325351; PubMed=7519448;
RA Geng Y.J., Almquist M., Hansson G.K.;
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Db 538 VLFATETGKSEALARDIAAL-FSYAFNTKVCMEQYKANTLEEEQLLLVVTSTFGNGDCP 596
Qy 542 DNAKOFVDWLDQASADEVKGV----RYSVFGCGDKNWTYYOKVPAP---IDETLAAKGA 594
Db 597 SNGCTL-----KSLFMKELGHTFRYAVFGLG-----SSMYPQCAFADIDOKLSHLGA 647
Qy 595 ENTIADRGEDASDDFEGTYEWEHMHWSVAAFNLDIENS-----ED 637
Db 648 SOLAPTGEDELSCQEDAFRSWAVQTFR--AACETFDVRSKHCIQIPKRYTSNATWEPEQ 705
Qy 638 NKSTLSLQFVDSAADMLAKMH--GAPSTNVVASKELQOPGSARSTR--HLEIETLPKEAS 693
Db 706 YKLTQSPESLD--LNKALSSIHAKNFTMLKSLQNLQSEKSSRTLLVQLTFEGSRGPS 763
Qy 694 YQEGDHGIVIPRNYEGIVNRVTARFGLDAS---QOIRLEAE---KLAHLPLAKTV 744
Db 764 YLPGHGLGIFPGNTALVOGILERV-VDCSSPDQTVCLVLEDESQYVWVKDKRLP----PC 819
Qy 745 SVELLOY-VELQDPVTRTOLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLLEL 803
Db 820 SLRQALTYFLDITTPPTQLQHLKAREATEETHRQLEALCQPSEYNDWKFSNNPTLEV 879
Qy 804 LEKYPACEMKFSEFIALLPSTIRPRYYSISSPRVDEKQASITYSVVSGEAWSGYGE-YKG 862
Db 880 LEEFPSLRVPAFLLSQLPIKPRYYSISSQDHTPSEVHLTVAVTYTRDQGGPLHHG 939
Qy 863 IASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVGPGTVAPFGFVQAR-KOLK 921
Db 940 VCSTWINNLKPEDVPVPCFVRS-VSGFOLPEDPSOPCILIGPGTGIAPFRSFWQORLHDSQ 998
Qy 922 EQQSGLGEAHLFGCRSPHEDYLYQELENAQSEGII-TLHTAFSRMPNQPKTYVOHVME 980
Db 999 HRGLKGRMTLVFGCRHPEEDHLYQEEMQENVRKGVLFQVHTGYSRPLPGPKVYVQDILQ 1058
Qy 981 QD-GKKLIELL--DOGAHFYICDGSOMAPAVEATLMKSYADYHVQVSEADARLWLOLEE 1037
Db 1059 KELADEVFSVLHGEQG-HLIVCGD--VRNARDVATLLAKLVAAKLNLSSEQVEDYFFOLKS 1116
Qy 1038 KGRYAKDVW 1046
Db 1117 QKRYHEDIF 1125

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Search completed: May 29, 2003, 08:29:01
 Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:25:36 ; Search time 99 Seconds
(without alignments)
2181.186 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TKEMPQPTFGELKNLPL.....RLWLOLEEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1736.5	31.8	1066	3 Q9Y8G7	Q9Y8G7 fusarium ox
2	1462.5	26.8	1115	3 Q9HGE0	Q9HGE0 gibberella
3	961	17.6	527	16 Q9RD76	Q9RD76 streptomyce
4	773.5	14.2	667	11 Q60451	Q60451 cricetus
5	745	13.7	719	10 Q40916	Q40916 pseudotsuga
6	739.5	13.6	692	10 Q9SB48	Q9SB48 arabidopsis
7	737.5	13.5	681	10 Q48937	Q48937 petroselinu
8	734.5	13.5	703	10 Q8VX49	Q8VX49 triticum ae
9	717	13.1	712	10 Q9AU06	Q9AU06 populus bal
10	714.5	13.1	692	10 Q39035	Q39035 arabidopsis
11	711.5	13.0	683	10 Q24424	Q24424 papaver som
12	711.5	13.0	692	10 Q9AU08	Q9AU08 populus bal
13	711	13.0	692	10 Q43235	Q43235 vicia sativ
14	710	13.0	656	10 Q9FVM7	Q9FVM7 triticum ae
15	709	13.0	711	10 Q9SUM3	Q9SUM3 arabidopsis
16	706	12.9	705	10 Q24425	Q24425 eschscholzi

ALIGNMENTS

RESULT 1

ID	Q9Y8G7	PRELIMINARY;	PRT;	1066 AA.
AC	Q9Y8G7;			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-hydroxylase) (P450foxy) [Includes: cytochrome P450 505 (EC 1.14.14.1); NADPH-cytochrome P450 reductase (EC 1.6.2.4)].			
GN	CYP505.			
OS	Fusarium oxysporum.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; mitosporic Hypocreales; Fusarium.			
OX	NCBI_TaxID=5507;			
RN	[1]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.			
RC	STRAIN-MT-811;			
RC	MEDLINE=20564350; PubMed=10995755;			
RA	Kitazume T., Takaya N., Nakayama N., Shoun H.;			
RT	"Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a membrane-bound eukaryotic counterpart of Bacillus megaterium cytochrome P450BM3.";			
RL	J. Biol. Chem. 275:39734-39740(2000).			
RN	[2]			
RP	FUNCTION, AND SUBCELLULAR LOCATION.			
RC	STRAIN-MT-811;			
RC	MEDLINE=96271003; PubMed=8830036;			
RA	Nakayama N., Takemae A., Shoun H.;			
RT	"Cytochrome P450foxy, a catalytically self-sufficient fatty acid hydroxylase of the fungus Fusarium oxysporum.";			
RL	J. Biochem. 119:433-440(1996).			
CC	-1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450.			
CC	-1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2O).			
CC	-1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2			

Q96561 helianthus
Q48938 petroselinu
Q39036 arabidopsis
Q04434 pisum sativ
Q92400 rhodococcus
Q9AU07 populus bal
Q9NKV3 bombyx mori
Q9R0W4 rattus norv
Q09590 caenorhabdi
Q9BDH6 equus cabal
P91655 drosophila
Q9HD32 phanerocha
Q9QW28 rattus sp.
Q9HG14 phanerocha
Q9HFV3 thizopus st
Q8R410 mus musculu
Q94904 homo sapien
Q97604 canis famill
Q00141 aspergillus
Q9C498 rhodotorula
Q9N175 ovis aries
Q8X1W0 coriolus ve
Q9K576 bacillus ha
Q32214 bacillus su
Q96560 helianthus
Q9P4E2 cunningham
Q968V4 physarum po
Q9WTK6 cavia porce
Q9TUX8 canis famill

17 705.5 12.9 588 10 Q96561
18 705 12.9 699 10 Q48938
19 702.5 12.9 712 10 Q39036
20 695.5 12.7 704 10 Q04434
21 694 12.7 321 2 Q92400
22 691 12.7 712 10 Q9AU07
23 690.5 12.7 687 5 Q9NKV3
24 685.5 12.6 1147 11 Q9R0W4
25 684.5 12.5 662 5 Q09590
26 681.5 12.5 1311 6 Q9BDH6
27 680 12.5 701 5 P91655
28 680 12.5 736 3 Q9HD32
29 669.5 12.3 1147 11 Q9QW28
30 668 12.2 690 3 Q9HG14
31 667.5 12.2 671 3 Q9HFV3
32 665.5 12.2 1145 11 Q8R410
33 661 12.1 1114 4 Q94904
34 658.5 12.1 1154 6 Q97604
35 657.5 12.0 693 3 Q00141
36 651.5 11.9 759 3 Q9C498
37 650.5 11.9 945 6 Q9N175
38 644.5 11.8 730 3 Q8X1W0
39 636.5 11.7 607 16 Q9K576
40 628.5 11.5 605 16 Q32214
41 627.5 11.5 506 10 Q96560
42 617.5 11.3 710 3 Q9P4E2
43 615.5 11.3 1055 5 Q968V4
44 605.5 11.1 1206 11 Q9WTK6
45 597.5 10.9 1205 6 Q9TUX8

CC FERROCYTOCHROME.
CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
DR EMBL: AB030037; BAA82526.1; -.
DR HSSP: P14779; IBVY.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR Pfam: PF00067; p450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
FT DOMAIN 1 480 CYTOCHROME_P450.
FT DOMAIN 481 1066 NADPH-P-450 REDUCTASE.
FT BINDING 407 407 HEME (BY SIMILARITY).
SQ SEQUENCE 1066 AA; 117925 MW; 6B8123698C23DBA CRC64;

Query Match 31.8%; Score 1736.5; DB 3; Length 1066;
Best Local Similarity 36.8%; Pred. No. 2.5e-100;
Matches 395; Conservative 190; Mismatches 444; Indels 43; Gaps 19;

QY 5 MPQKTFGKLNPLINTDKPQVQALADELGEIFKFEAPGRVTRVYLSQRLIKEACDE 64
DB 7 IPEPPCYPLIGNLGEF-TSNPLSDLNRLADTVGPIFRLRLGAKAPFVSSNSLINEVCE 65
QY 65 SRFDKLSALAEVRDFADGDLFTSWHEKNKKAHNILLPSFSQAMKGYHAMVDAIV 124
DB 66 KRPFKTLKSVLSQVRHGVHDFTAFEDPEPNKGAKHRLVPAFGLSIRGMPPEMHDIAT 125
QY 125 QLVQKWERLNADHEHVEPDMTRLATDTIGLCGFNYRFSFYRDOQPHPTISWALDIA 184
DB 126 QLCMKFARGPRTPIDTSNFTRLADTLALCAMDFRYSYKEELHFPFEANGDFLES 185
QY 185 MNKLGARNDPDP--AYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNGKD 242
DB 186 GNR-NRRPPFAPNFYRAANERFYGDIALKMSVADEVVAARAKSPSDRDKLLAAMNGVD 244
QY 243 PETGPELDDENTRYQILITFLIAGHETTSCLLSFALYFLVKNPHVLOKAAEAAEAVLVDPV 302
DB 245 PGTGKLSDNITNQLITFLIAGHETTSGTSLSFAMYQLLNPEAYSKVQKEYTVVGRGP 304
QY 303 PSYQVQKQLYGVGMVLEALRWPTAPAFSLYAKEDTVLGGYPLEKGGDELMLVLIPQLHR 362
DB 305 VLVEHLTKLPYISAVLRETFLRLNSPTAFGLEAIDDTFLGGKLYLKKEIVTALLSRGHV 364
QY 363 DKTINGDDVEEPRPER-----PENPSAIPQHAFAKFPFGNGQACIGQQFALHEATVLVGM 417
DB 365 DPVVTGNDADKFIPEMLDDEPARLNKEYPNCKPFGNGKACIGRPFAWQBSLLAMVYL 424
QY 418 LKHFDPE-DHTNYELDKETLTKPEGFVWAKSKK-----IPLGGTIPSPSTQSS 466
DB 425 FQNFMTWDPNYYALEIKQTLLTKPDHFIYINATLRHGMTPTLEHVLNAGNAGNCSSTNI 484
QY 467 AKKVRKKAENAHNTPLLVLYGSMGTAGTARDLADIAMSKGF-APOVATLDSHAGNLP 525
DB 485 KAAANLDKAGSKGPMATFYGSNGTCEALANRLASDAPSGFSTATTGDLDDQAKONLPE 544
QY 526 EGAVLIVTASYNCHPPDNAQFVDLQDASADKGVRYSVFGCGDKNWTATYQVPAFI 585
DB 545 DRPVVIVTASVYBGQPPSNAAHFIKWNEDLDGNDMEKVSYAVFACGHHWDVETFRIPKLV 604
QY 586 DDTLAAKGAENTADRGAD-ASDDFEGTYEWEH-HMWSDVAAAYFNLDIENSNDKSTLS 643

DB 605 DSTLEKRGCTRLVPMGSDAATSDMFDEAWEDIVLWPLGKEKYKISDEESGGQKGLL- 663
QY 644 LQFVDSADMPKAKMHGAFSTNVASKELQPGSARSTRHLEIEPKESYQEGHGLGYI 703
DB 664 ----VEVSTPRKTSLRQDVEEALVVAEKTTLTKSGPAK--KHIEIQLPVSAMTYKAGDYLA 718
QY 704 PRNYEGIVNRVTRFGLDASQOIRLEAEKEKLAHLPLAKTVSVVEELLQ-YVELQDPVTRT 762
DB 719 PLNPKSTVARVFRFRELAWDSFLKIQSEGP--TTLPTNVAISAFDVSAYVELSQPATKR 776
QY 763 QLRMAAKTVCPPHKVELEALLEKQAYKEQVLAKRITMLLELLEKYPACEMKTFSEFIALP 822
DB 777 NILALAEATEDKDTIQELER-LAGDAYQAEISPKRVSVLDLLEKFPALPFISSYLAMP 835
QY 823 SIRPRYISSTSPRYDEKQASITVSVSGEANSYGVGEYKGIASNYLAELQEGDTTCFIS 882
DB 836 PMRVQYISLSSPFADPDKLTITLYSLDAPSLSGQRHVGVATNLFSLHUTAGDKLHVSVR 895
QY 883 TPQSEFTLPKDPPE-TPLIMVPGTGVAPFRGFVQARKQKQEQQSILGEAHLFYGCSPHE 941
DB 896 ASSEAFHLPDAEKTPIICVAAAGTGLALRGFIQERAAMLAAGRTLAPALLFFGCRNPEI 955
QY 942 DYLYQEELENAQSEGIITLHTAFSRMPNPK--TVYQHVMEODGKKLELLDQGAHFYIC 999
DB 956 DDLYAEFEFERWEKMGAVDVRRAYSRATDKSECKYQDVRVYHADRADVKVMDQGAHVFC 1015
QY 1000 GDSQWAPAVE-----ATLMKSYADVHVSEADARLWLQOLEEGKRYAKDVW 1046
DB 1016 G-SREIGRAVEDVCVRLAIEKAQQQRDVTEEMARANFERSRNE-RFATDVF 1065

RESULT 2
Q9HGE0
ID Q9HGE0 PRELIMINARY; PRT; 1115 AA.
AC Q9HGE0
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Fum6p.
GN FUM6.
OS Gibberella moniliformis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocerales; Nectriaceae; Gibberella.
OX NCBI_TaxID=117187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-3125;
RA Proctor R.H., Seo J.-A., Plattner R.D.;
RT "Characterization of four clustered and coregulated genes associated
RT with fumonisin biosynthesis in Fusarium verticillioides";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF155773; AAG27132.1; -.
DR HSSP: P00388; 1J9Z.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR Pfam: PF00067; p450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 1115 AA; 123276 MW; 5C6D2B947AE86C25 CRC64;

Query Match

26.8%; Score 1462.5; DB 3; Length 1115;


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Db 64 PKSLMAKDEDDLDLG-----SGKTRVSIFFGTGTGTAGFAKAL 103
QY 501 AD--IAMSKGFAPOVATLDLHAGN-----LPREGAVLIVTASY-NGHPPDNNAKORVDW 550
Db 104 SEETKARYEAAVKVVDLDYADDDOYEKLEKETAFCVATYVGDGETDNNARYKW 163
QY 551 LQASADEVK--GVRSVFCGDKNNWATYQKVPAFIDETLAAGAENIADRGAEADSD 608
Db 164 FTEENERDIKLOLAYGVFALGNQY-EHENKIGIVLDEELCKGAKRLIEVGLGDDQS 222
QY 609 FEGTYEENRHMSSDAAYFNLD- IENSEDNKS-----TSLIQ 645
Db 223 IEDDFNAWKESLWSE-----LDKLLKDEDDKSVATPYTAIPEYRVVTHDPRFTQKSM 276
QY 646 FVDSADMDPLAKMHGAFSTNVVASKELQOPGSASTRHLIELPKEA-SYQEGDHLGVIP 704
Db 277 ESNVANGNTIDIHFCRCVDVAQVKELHTHESRSCIHLEFDISRTGITTYETGDHVGVA 336
QY 705 RNYEGIVNRVTARFGLDASQIIRLEAEELKLAHLPLAKTVSV-----EELLOYVEL 755
Db 337 ENHVEIVEEAGKLLGHSLLDVFESIHADKEDGS--PLESAVPPPPPGPCTLGTGLARYADL 394
QY 756 QDPVTRTOLRAMAAKTVCPHPKVELEALLE---KQAYKEQVLAKRLTLMLELKYIPACEM 812
Db 395 LNPPRSALVALAAYATEPSEAEKHLKHLTSPDGKDEYSQWIVASQRSLLLEVMAAFPSAKP 454
QY 813 KFSEFT-ALLPSIRPRYSSISPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL--- 868
Db 455 PLGVFAAIAIAPRQPRYSSISPRPLASRVHVTSLVYPTTG-RIHKGVCSTWKNNA 513
QY 869 ---AELQEGTITCFSTPQSEFTLPKDPETPLIMVPGTGVAPFRGFVQARKOLKEQG 925
Db 514 VPAEKSHESGAPFIRA--SNEKLPSPSTPIVMVPGTGLAPFRGFQERMAKLEDGE 571
QY 926 SLGEAHLYGCRSPHEDLYQOELENAQSEGIIT-LHTAFSRMPNPQKTYVQHVMEQDGK 984
Db 572 ELGSSLLFFGCRNRQMDFIYEDELNNFVDQGVISELIMAFSREGAO-KETVQHKMEKAA 630
QY 985 KLIELLDQGAHFYICGDSQMAPAVEATLMKSYADYVQVSEADARLWLOOLEKRYAKD 1044
Db 631 QVWDLIKEGYLVCGDAKGMARDVHRTLHTIIVQEGEGYSSSEAEIIVKKLQTEGYLRD 690
QY 1045 VW 1046
Db 691 VW 692

RESULT 7
O48937 ID O48937 PRELIMINARY; PRT; 681 AA.
AC O48937;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADPH cytochrome P450 reductase (EC 1.6.2.4).
GN CPR2.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxId=4043;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98070859; PubMed=9405720;
RA Koopmann E., Hahlbrock K.;
RT "Differentially regulated NADPH:cytochrome P450 oxidoreductases in
RT parsley.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:14954-14959(1997).
DR EMBL; AF024634; AAB97736.1; -.
DR HSSP; P00388; IAM0.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
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DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase.
SQ SEQUENCE 681 AA; 75674 MW; C67AD80E8BAE0F6 CRC64;

Query Match 13.5%; Score 737.5; DB 10; Length 681;
Best Local Similarity 30.7%; Pred. No. 7.4e-38;
Matches 200; Conservative 104; Mismatches 275; Indels 73; Gaps 18;

QY 449 KSKKIPGLGIPSPSTEQSAKKVKKKAENAHNTPLLVLYGSMGTACTGARDLADIAMSGK 508
Db 49 KSEVPKLIYPRKVIIEDEVDGKKK-----VTVFQGTGTAGFAFAFAEAKARY 100
QY 509 FAP--OVATLDLSDA-----GNLPREGAVLIVTASY-NGHPPDNNAKQFVDWLDQA--SA 556
Db 101 ERAKFRVVDLDDYAADEDEYEAKFKKESPAFFLATYGDGETDNNARFYKWFSEBEKG 160
QY 557 DEYGVYRSYVFCGDKNNWATYQKVPAFIDETLAAGAENIADRGAEADSDDFEGTYEEW 616
Db 161 DWLNLQYGVFGLGNQY-EHENKIAKVVDDGLADQAKRIVEVGMGDDDOCIDEDDTAW 219
QY 617 REHMSD-----VAAYFNLDIENSEDNKSTLSLQFVDSAA 651
Db 220 RELVWPELKLLEDDETSAATPYTAALVLEYRVVVDQDLDATFLDSLSTQNGHTVHDA- 278
QY 652 DMLAKMHGAFSTNVVASKELQOPGSASTRHLIELPKEA-SYQEGDHLGVIPRIVEGI 710
Db 279 -----QHPCRS-SVAAKKELHKPADRSCHILEFDISHTGLAYETGDHVGVCENLVEI 331
QY 711 VNRVTARFGLDASQITRLEAEKLAHL-----PLAKTVSVEELLYQVLEODPVTRTQ 763
Db 332 VEEAEKLLGMQNPYTSVHIDDEDGTPLAGGSLPPPPPPCTVRSALAKYADLLSPKKA 391
QY 764 LRMAAAKTVCPHPKVELEALLE---KQAYKEQVLAKRLTLMLELKYIPACEMKFSFIA- 819
Db 392 LIALAAHSDPTEADRLRLASDPAGDEYAQWVASHRSLLEVLAEFFSAKPLPLGVFFAS 451
QY 820 LLPSIRPRYSSISPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL---AELQEG-D 875
Db 452 VAPRLQPRYSSISPRVPSRIHVTALVYKPTTG-RIHKGVCSTWKNNAVSLEESHD 510
QY 876 TITCFITPQSEFTLPKDPETPLIMVPGTGVAPFRGFVQARKOLKEQGSGLGEAHLYFG 935
Db 511 CSWAPIFVRSQSNFKLPSTKVPITMIGTGLAPFRGFLQERQALDAGAEGLTAVLYFG 570
QY 936 CRSPHEDLYQOELEN-AQSEGIITLHTAFSRMPNPQKTYVQHVMEQDGKLLLELDQGA 994
Db 571 CNRNLDIFYEDELNKFVSGSISELIVAFSR-EGTKEYVQHKMLQKASEIWNLLISEGA 629
QY 995 HFYICGDSQMAPAVEATLMKSYADYVQVSEADARLWLOOLEKRYAKDW 1046
Db 630 YIYVCGDAKGMARDVHRLHTIAEQOGLDSSKAESWKNLQMTGRLYLRDW 681

RESULT 8
O8VX49 ID O8VX49 PRELIMINARY; PRT; 703 AA.
AC O8VX49;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome P450 reductase (EC 1.6.2.4).
GN R2.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
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Db 601 GCNRKMDFYEDLNINNVESGALSELVAFSR-EGPTKEYVQHKMKASDINNISQ 659
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSEADARLWLQOLKEKGRIKADYV 1046
Db 660 GYLXVCGDAKGMADVHRALHTIVQEGSLDNSTESFVKSLOMNGRYLDDW 712

RESULT 10
QY 93035 PRELIMINARY; PRT; 692 AA.
ID Q39035
AC Q39035
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADPH-ferrihemoprotein reductase.
GN ATR1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEYNH; TISSUE=SEEDLING;
RA Mignote-Vieux C., Kazmaier M., Lacroute F., Pompon D.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X65016; CA446814.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW NADP.
SQ SEQUENCE 692 AA; 76768 MW; 5E0216F008B5D49E CRC64;

Query Match 13.1%; Score 714.5; DB 10; Length 692;
Best Local Similarity 29.2%; Pred. No. 2.1e-36;
Matches 193; Conservative 119; Mismatches 261; Indels 89; Gaps 19;

QY 441 PEGVYVAKSKKIPLGIPSPSTEQSAKVRKKAENAHNTPLLVLYGSGNMGTAEGRDIL 500
Db 64 PKSLMAKDEDDLDLG-----SGKTRYSIFFGTGTGTAEGRFALKAL 103

QY 501 AD--IAMSGFAPQVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDNNAKQFVDM 550
Db 104 SEBIKARYEKAQVAVVLDLDYAADDDQYBEKLLKETLAFVCVATYGDGPTDNNARFSKW 163

QY 551 LQASADEVK--GVRYSVFGCGDKNATYQKVPATIDETLAAKGAENIADGEADSD 608
Db 164 FTEENEDRLQOLATGVFALGNQY- EHFNKIGIVLDEELCKKAKRLIEVLGLGDDQS 222

QY 609 FEITYEWEHWMSSDVAAYFNLD- IENSDNKS-----TSLQ 645
Db 223 IEDDFNAKESLWSE-----LQKLLKDEDDKSVATPYTAVIPEYRVVTHDPRFTQKSM 276

QY 646 FVDSADNMLAKMHGAFSTNVVASKELQOPGSGARSTRHLEIPLKEA-SYQEGDHLGVTP 704
Db 277 ESNVANGNTTIDHPCRYDVAVQKELHTHESDRSCIHFLEFIDISRTGITETGDHVGYYA 336

QY 705 RNYEGVNVNRTARFGDASQIRLEAEKLAHLPLAKTVSV-----ELLQYVEL 755
Db 337 ENHVEIVEAGKLLGSLDLSVSIHADKEDGS--PLESVPVPPPGPCITGLGLIADL 394

QY 756 QDPVTRQLRAAMAKTVCPHPHVELLEALLE---KQAYKEQVLAKRLTLMLELLEKYPACEM 812
Db 395 LNPPRKSALVALAAYATEPSEAEKLLKHLTSPDGKDEY SQWIVASQSLLEVMAAFPSAKP 454
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QY 813 KFSEFI-ALLPSIRPRIYSISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYL--- 868
Db 455 PLGVFFAAATAPRLQPRYSSISSCQDWPASRVHVTYSALVYPTTG-RIHKGVCSTWKNKA 513
QY 869 ---AELOEGDITTCFISTFQSEFTLPKDPETPLIMVPGTGVAPPFGFVQARKLKEQ 925
Db 514 VPAKSHCEGSGAPIFIRA--SNFKLPSPSTPIVMVPGTGLAPFRGFLQERNALKEDGE 571
QY 926 SLGEAHLVFGCRSPHEDLYOELENAQSEGIIT-LHTAFSRMPNPKTYVQHVMSQDGK 984
Db 572 ELGSSLLFFGCRNRQMDFIYEDLNINNVQGVISELIMAFSREGAQ-KEYVQHKMEKAA 630
QY 985 KLIELDQGAHFYICGDSQMAPAVEATLMKSYADVHOVSEADARLWLQOLKEKGRIKAD 1044
Db 631 QVWDLIKEGYLVCGDAKGMADVHRHTLHTIVQEGVSSSEAEIVKKIQTEGRLD 690
QY 1045 VW 1046
Db 691 VW 692

RESULT 11
QY 024424 PRELIMINARY; PRT; 683 AA.
ID 024424
AC 024424
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADPH-ferrihemoprotein oxidoreductase (EC 1.6.2.4).
OS Papaver somniferum (Opium poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Papaver.
OX NCBI_TaxID=3469;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98096363; PubMed=9434750;
RA Rosco A., Pauli H.H., Priesner W., Kutchan T.M.;
RT "Cloning and heterologous expression of NADPH-cytochrome P450
RT reductases from the Papaveraceae.";
RL Arch. Biochem. Biophys. 348:369-377(1997).
DR EMBL; U67185; AAC05021.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase.
SQ SEQUENCE 683 AA; 75888 MW; E07BD5E5EA8DE002 CRC64;
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Query Match 13.0%; Score 711.5; DB 10; Length 683;
Best Local Similarity 30.3%; Pred. No. 3.2e-36;
Matches 191; Conservative 113; Mismatches 263; Indels 63; Gaps 20;

QY 470 VRKKAENAHNTP-----LLVLYGSGNMGTAEGRDLDAD--IAMSGFAPQVATLDSHAG-- 521
Db 64 IDKEEEIEIEVPGKIKLTIFGTGTAEGRFAKALAEIKAKYKKAIVKVVLDLDDYAAD 123

QY 522 -----NLREGAVLIVTASY-NGHPDPNNAKQFVDMLDQ--ASADEVKGVRYSVFGCGDKN 573
Db 124 DQYEKLLKESLVFFWATYGDGPTDNNARYKKNFTQEHERGEWLQOITYGVFGLGNQ 183

QY 574 WATTYQKVPATIDETLAAKGAENIADGEADSDDPFEGTYEWEHWMSSD----- 623
Db 184 Y-EHFENKIAVDVDEQLGKQAKRIVQVGLGDDQCIEDDFTAWRELLWTELQDLKDEDA 242

QY 624 -----VAAFNLDIENSEDNKSTLSLQFVDSA-ADMLAKMHGAFSTNVVASKELQ 674
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Db 243 APSVATPIATVPEYRVVHETTTVAALDDKHINTANGDVAFDILHPC-RTIIVAQOQRELHK 301
QY 675 PGSARSTRHLEIELP-KEASYQBGDHLGVIPRNVGIVNRTARFG--LDASQOIRLEAE 731
Db 302 PKSDRSCHLEHFEIDISGSLTYEGDVGVAENCDTEVEAGKLGLGPDLLFSIHTDKE 361
QY 732 EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQLRAMAAKTVCPPHKEVELEA 782
Db 362 DGS-----PQSSSLPPPPGPGCTLSALARYADLLNPPKASLIALSAHASVPSEAEARLRF 417
QY 783 L---LEKQAVKEOVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYISYSSSPRVD 838
Db 418 LSSPLGKNEYSKVVGSQSSLLIEAEFFSAKPLPLGVFFAAVAPRPPRYISYSSSPKFA 477
QY 839 EKQASITVSVSGEAWSGYGEYKGIASNYLAELQEGDT-ITCFITSPQSEFTLPKOPETP 897
Db 478 PSRIHYTCALVYGOSTPG-NVHRGVCSTWKKHVPQDSWAPIFVRT--SNFKLPADSTP 534
QY 898 LIMVPGGTGVAPRFGFVQARKQKQOQSLGEAHLPGCRSPHEDYLYOELENAOSEGI 957
Db 535 IIMVPGTGLAPRFGFLOERMAKNGAQLGPAVLFPGCRNRMDFIYEDLNFRVGV 594
QY 958 IT-LHTAFSRMPNQPRTYVQHVMEQDKKLIELLDQGAHEYICGDSQMAPAVEATLMKS 1016
Db 595 ISELVAFSR-EGEKKEYVOHRKMKATDVNMVNSGDYLYVCGDAKGMAVDVHRTLHTI 653
QY 1017 YADVHVSEADARLWLQLEEKGRYAKDVW 1046
Db 654 AQOGPNSESSAAEAANKLQVEERYLRDWM 683

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RESULT 12

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Q9AU08 PRELIMINARY; PRT; 692 AA.
ID Q9AU08 Q9AU08
AC Q9AU08 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADPH-cytochrome P450 oxidoreductase isoform 1.
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3695;
RN [1]
RP SEQUENCE FROM N.A.
RA RO D.-K., Douglas C.;
RT "Functional characterization of cytochrome P450 reductase from the
RL hybrid poplar (Populus trichocarpa x P. deltoides).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF302496; AAK15259.1; -
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 692 AA; 76725 MW; 7AA8CC78B3C984D9 CRC64;

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Query Match 13.08; Score 711.5; DB 10; Length 692;
Best Local Similarity 28.9%; Pred. No. 3.3e-36;
Matches 199; Conservative 110; Mismatches 252; Indels 127; Gaps 20;
QY 431 LDKETLTLKPEGVVKAASKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLVLVGSNM 490
Db 60 LVVPKLSIRKDE-----EDESEALGG-----KTKVTFYGTQT 92

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QY 491 GTAEGTARDLAD--IAMSKGFAQVATLDSHA-----GNLPREGAVLIVTASY-NGHP 540
Db 93 GTAEQFALAAEEVKAREKAAVKVFDLDDYAMEDDDQYEEKLKKETLALFMVATYGDGP 152
QY 541 PDNAKQFVMDQASADEV--KGVRYSVFGCGKNWATYQKVPAFIDETLAAKGAENIA 598
Db 153 TDNAARPKYKFTGNEGRGIWLQQLSYGVFGNROY-EHFNKIAKVILDDLLYEQGGKRLV 211
QY 599 DRGEADADDQFEGYEWEHREHMVSDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLA-- 656
Db 212 PVGLGDDQDIEDDFSAAKEFLWPELD-----QLLRDEDDVNAPSTPYTAIPEYRLVIH 266
QY 657 -----KMGAFSTNVASKELQOQSGASRTHLELELPEKA-SY 694
Db 267 DPSIISVEDKFSLANGNVSFDIHPCRVNVAVQKELHKAESDRSCIHLEFDITGTITY 326
QY 695 QEGDHLGVIPRNVGIVNRTARGLDASQOIRLEAEKEEKLHPLAKTVSVE-----747
Db 327 ETGDLGVYAENSETVE-----EAGKLLDKPLDLLFSIHADNEDGT 368
QY 748 -----ELLQYVELQDPVTRTQLRAMAAKTVCPPHKEVELEAL--K 786
Db 369 AIGSSLPPPPGPGCTLHTALACYADLLSPPKAALLAALAAHASEPSEADRLKFLSSPGK 428
QY 787 QAYKEQVLAKRLNMLELEKYPACEMKFSEFI-ALLPSIRPRYISYSSSPRVDKQASIT 845
Db 429 NEYSHWYNASQSLLEVMAEFPSPKPLGIFFAVAPRLOPRYISYSSSPRYTNRVHT 488
QY 846 VSVVSGEAWSGYGEYKGIASNYL--AELQEGDTITCF---ISTPQSEFTLPKOPETPLI 899
Db 489 CALVYGTPGTG-RIHKGVCSTWKKHVPQDSWAPIFVRT--SYECWAPIFRTSNFKLPADSTPII 545
QY 900 MVGPGTGVAPRFGFVQARKQKQOQSLGEAHLPGCRSPHEDYLYOELENAOSEGIT 959
Db 546 MVGPGTGLAPRFGFLOERMAKNGAQLGPAVLFPGCRNRMDFIYEDLNFRVGV 605
QY 960 -LHTAFSRMPNQPRTYVQHVMEQDKKLIELLDQGAHEYICGDSQMAPAVEATLMKSYA 1018
Db 606 ELIVAFSREGPQ-KEYVQHKMVDRAAEITWISQGYFYVCGDAKGMAVDVHRTLHTIVQ 664
QY 1019 DVHQVSADARLWLQLEEKGRYAKDVW 1046
Db 665 EQGLDSSKTESMVKLQMEGRYLRDWM 692

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RESULT 13

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Q43235 PRELIMINARY; PRT; 692 AA.
ID Q43235 Q43235
AC Q43235 2001 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADPH-ferrihemoprotein reductase (EC 1.6.2.4).
OS Vicia sativa (Spring vetch) (Tare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicia;
OX NCBI_TaxID=3908;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VAR. LOLITA; TISSUE=SEEDLING;
RA Benveniste I., Begue-Kirn C., Lesot A., Hasenfratz M., Durst F.;
RT "Isolation and characterization of a cDNA encoding an NADPH-cytochrome
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26252; CAA81211.1; -
DR HSSP; P00388; Iu92.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.

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649 GRYLRDVG 656
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QY 602 EADSDDFEGTYEWEHMSDV-----AAENLDIENSEDNKSTL 642
DB 236 LGDDDOCIEDDTANREALWPELDTILREEGDTAVATPYTAALVYRVSJHSEDAKFN- 294
QY 643 SIQFVDSAADPLAKMHG-----AFSTNVVASKELQOPGSGARSTRHLELPEKA-S 593
DB 295 -----DINMANGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSLT 345
QY 694 YQEGDHLGVIIPRYEGIVNRVTRFGLDASQQIRLEAEKEKLAHLPLAKTVSV----- 746
DB 346 YETGDHVGVLCDNLSETVDEALRLDMSPTVYSLHAEKD--GTPISSLPFPFPCNL 403
QY 747 -BELIQVLELQDPVTRTQLRAMAAKTVCPHPKVELEALLE---KQAYKEQVLAKRUTMLE 802
DB 404 RTALRYACLLSSPKSALVALAAHSDPTEARLKLHASPCKDEYSKWVYESQRSLLLE 463
QY 803 LLEKYPACEMKFSEFTA-LLPSIRPRYYSISSPRVDEKQASTVSVSGEAMSGYGEYK 861
DB 464 VNAEPSPAKPPLGCVFAGVAPRLQPRFYSSSPKIAETRIHVTCALVYEKMTG-RIHK 522
QY 862 GTASNYLAELQEGDTITCFISTP-----QSEFTLPKDPETPLIMVGPCTGVAPERGVOAR 917
DB 523 GVCSTWKNNAVPEYKSENCSSAPIFVYRQSNFKLPDSKVPITIMIGPTGLAPRGLQER 582
QY 918 KOLKEQGQSLGEAHLFGCRSPHEDYLYOELEN-AQSEGIITLHTAFSRMPNQKTYVQ 976
DB 583 LALVESGVELGPSVLEFGCRNRRMDFIYEELQRFVESGALAEISYAFSR-EGPTKEYVQ 641
QY 977 HVMEOQDKKLIELDQGAHFYICGDSQMAPAVEATIMKSYADHVQVSEADARLWLOOLE 1036
DB 642 HKMMDKASDIWNMISQAYLYVCGDAKGMARDVHRSILHTIAQPGSGMDSTKAEQGVKNLQ 701
QY 1037 EKGRYAKDYW 1046
DB 702 TSGRYLRDVG 711
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Search completed: May 29, 2003, 08:30:49
Job time : 104 secs

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649 GRYLRDVG 656
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QY 602 EADSDDFEGTYEWEHMSDV-----AAENLDIENSEDNKSTL 642
DB 236 LGDDDOCIEDDTANREALWPELDTILREEGDTAVATPYTAALVYRVSJHSEDAKFN- 294
QY 643 SIQFVDSAADPLAKMHG-----AFSTNVVASKELQOPGSGARSTRHLELPEKA-S 593
DB 295 -----DINMANGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSLT 345
QY 694 YQEGDHLGVIIPRYEGIVNRVTRFGLDASQQIRLEAEKEKLAHLPLAKTVSV----- 746
DB 346 YETGDHVGVLCDNLSETVDEALRLDMSPTVYSLHAEKD--GTPISSLPFPFPCNL 403
QY 747 -BELIQVLELQDPVTRTQLRAMAAKTVCPHPKVELEALLE---KQAYKEQVLAKRUTMLE 802
DB 404 RTALRYACLLSSPKSALVALAAHSDPTEARLKLHASPCKDEYSKWVYESQRSLLLE 463
QY 803 LLEKYPACEMKFSEFTA-LLPSIRPRYYSISSPRVDEKQASTVSVSGEAMSGYGEYK 861
DB 464 VNAEPSPAKPPLGCVFAGVAPRLQPRFYSSSPKIAETRIHVTCALVYEKMTG-RIHK 522
QY 862 GTASNYLAELQEGDTITCFISTP-----QSEFTLPKDPETPLIMVGPCTGVAPERGVOAR 917
DB 523 GVCSTWKNNAVPEYKSENCSSAPIFVYRQSNFKLPDSKVPITIMIGPTGLAPRGLQER 582
QY 918 KOLKEQGQSLGEAHLFGCRSPHEDYLYOELEN-AQSEGIITLHTAFSRMPNQKTYVQ 976
DB 583 LALVESGVELGPSVLEFGCRNRRMDFIYEELQRFVESGALAEISYAFSR-EGPTKEYVQ 641
QY 977 HVMEOQDKKLIELDQGAHFYICGDSQMAPAVEATIMKSYADHVQVSEADARLWLOOLE 1036
DB 642 HKMMDKASDIWNMISQAYLYVCGDAKGMARDVHRSILHTIAQPGSGMDSTKAEQGVKNLQ 701
QY 1037 EKGRYAKDYW 1046
DB 702 TSGRYLRDVG 711

Query Match 13.0%; Score 709; DB 10; Length 711;
Best Local Similarity 28.4%; Pred. No. 4.9e-36;
Matches 190; Conservative 120; Mismatches 264; Indels 96; Gaps 20;

QY 434 KETLTKPEGVVYKAKSKIPGLGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSGNWGA 493
DB 81 KRVEPLKP--LVIKPREEDDGG-----RRK-----VTIFFGTGTGTA 116
QY 494 EGTARDLADTAMSGFAP--QVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDN 543
DB 117 EGFALGEEAKARYEKTRFKIVDLDDYAADDDEYEELKKEDVAFFFLATYGDGEPTDN 176
QY 544 AKQFVWLDOAS--ADEVKGVRYSVFGCGDKWATYQKVPFIDETLAAKGAENTADRG 601
DB 177 AARFYKWFTEGDRGEWLNKLYGVFLGNROY-EHFNKVKAKVVDVDDILVEQGAORLVQVG 235
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